

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:10:08 ; Search time 6058.98 Seconds

(without alignments)

3720.338 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
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| 1 | 1247 | 100.0 | 708 | 2 | CQ882036 Sequence |
| 2 | 1247 | 100.0 | 708 | 2 | AX764523 Sequence |
| 3 | 1247 | 100.0 | 773 | 2 | BD226429 Immunosp |

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| 18 | 1166.5 | 93.5 | 2411 | 2 | DD211089 |
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ALIGNMENTS

RCT from same provisional

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| RESULT 1 | CQ882036 | Sequence 28 from Patent WO2004083404. | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| LOCUS | CQ882036 | | | | | |
| DEFINITION | CQ882036 | | | | | |
| ACCESSION | CQ882036 | | | | | |
| VERSION | CQ882036.1 | GI:54034749 | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | | | | | | |
| AUTHORS | Qi, Y., Zhang, X. and Konigsberg, P.J. | | | | | |
| TITLE | Gene therapy vectors having reduced immunogenicity | | | | | |
| JOURNAL | Patent: WO 2004083404-A 28 30-SEP-2004; | | | | | |
| ISOGNIS | Isogenis, Inc. (US) | | | | | |
| FEATURES | | | | | | |
| source | Location/Qualifiers | | | | | |
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ORIGIN

Alignment Scores:

Pred. No.:

Score:

6.84e-91

1247.00

Length:

708

Matches:

235

Kelly, R.
10/304763 page 1
Seq. ID 1-3

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| Best Local Similarity: | 100.0% | Mismatches: | 0 |
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US-10-804-763-1 (1-235) x CQ882036 (1-708)

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| Qy | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
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| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 121 | CTGAAGTGCCAGGTGCTGCTCCACCCGACGTGGGCTGCTGTGGCTCTTCCAGCGG | 180 |
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| Qy | 101 | ThrLeuSerAspPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 120 |
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| Qy | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 |
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| Qy | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| Db | 421 | CCAGCGCGCGACCAACACCGCGGCGCCACCATCGCGTCCGAGCCCTGTCCCTGCGC | 220 |
| Qy | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla | 180 |
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| Qy | 201 | ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro | 220 |
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ORIGIN

Alignment Scores:

Pred. No.: 6.84e-91 Length: 708

Score: 1247.00 Matches: 235

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

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Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

Db 181 CGCGGCGCGCGCGCTTCCGCGGAGACGAGGGCTACTATTCTGCTGGCCCTTGAGC 240

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Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180

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Db 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGGAGCTTGTGGGGTCTTCTCTCTGTC 260

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220

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FEATURES

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LOCUS

Sequence 40 from Patent WO02102852.

ACCESSION

AX764523.1

VERSION

AX764523.1

KEYWORDS

GI:32258731

SOURCE

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ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1

Jakobsen, B.K. and Glick, M.

Modified CD8 molecule, nucleic acid encoding said molecule, and

their therapeutic use

Patent: WO 02102852-A 40 27-DEC-2002;

Avindex Limited (GB)

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LOCUS Immunosuppression by blocking T cell co-stimulatory signal 2
DEFINITION (B7/CD28 interaction).
ACCESSION BD226429
VERSION BD226429.1 GI:33036199
KEYWORDS JP 2002513568-A/8.
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS Lechler,I.R. and Dorling,A.
TITLE Immunosuppression by blocking T cell co-stimulatory signal 2
JOURNAL (B7/CD28 interaction)
COMMENT Patent: JP 2002513568-A 8 14-MAY-2002;
IMPERIAL COLLEGE INNOVATIONS LTD
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PD 14-MAY-2002
PF 30-APR-1999 JP 2000547221
PI 30-APR-1998 GB 9809280.2
PR IAN ROBERT LECHLER,ANTHONY DORLING
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ACCESSION AX011079
VERSION AX011079.1 GI:9997709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Dorling,A. and Lechler,I.R.
TITLE Immunosuppression by blocking t cell co-stimulation signal 2
JOURNAL (b7/cd28 interaction)
Patent: WO 9957266-A 16 11-NOV-1999;
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Db 37 ATGGCTTACAGTGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCGAGG 96
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| Qy | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
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| LOCUS | | | |
| DEFINITION | Sequence 11859 from Patent WO02068579. | | |
| ACCESSION | CQ725925 | | |
| VERSION | CQ725925.1 | GI:42287423 | |
| KEYWORDS | | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | |
| | Hominidae; Homo. | | |
| REFERENCE | | | |
| AUTHORS | Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W. | | |
| TITLE | Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof | | |
| JOURNAL | Patent: WO 02068579-A 11859 06-SEP-2002; | | |
| FEATURES | PE Corporation (NY) (US) | | |
| source | Location/Qualifiers | | |
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| Pred. No.: | 9,94e-91 | Length: | 1059 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |

| | | | | |
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| Pred. No.: | | 9.95e-91 | Length: | 1060 |
| Score: | 1247.00 | Matches: | 235 | |
| Percent Similarity: | 100.0% | Conservative: | 0 | |
| Best Local Similarity: | 100.0% | Mismatches: | 0 | |
| Query Match: | 100.0% | Indels: | 0 | |
| DB: | 2 | Gaps: | 0 | |
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| QY | 1 | MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg | 20 | |
| Db | 66 | ATGGCCTTACCAGTACCGCCTTGCTCCGCGCTGGCTTGTCTCCACGCCGACG | 125 | |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 | |
| Db | 126 | CCGAGCCAGTTCGGGGTTCGGATCGGACCTGGAACTGGCGGAGACAGTGGAG | 185 | |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAenProThrSerGlyCysSerTrpLeuPheGlnPro | 60 | |
| Db | 186 | CTGAAGTGCAGGTCTGCTCCAAACCGAGTCGGGCTGCTCGTGGCTCTTCCAGCCG | 245 | |
| QY | 61 | ArgGlyAlaAlaSerProThrPheLeuLeuLeuSerGlnAsnLysProLysAla | 80 | |
| Db | 246 | CGCGGGCGCGCCAGTCCACCTTCTCTATACCTTCCAAACAGCCCAAGGCG | 305 | |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyValLeu | 100 | |
| Db | 306 | GCGGAGGGCTGACACCCAGCGGTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTC | 365 | |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 | |
| Db | 366 | ACCTTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC | 425 | |
| QY | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr | 140 | |
| Db | 426 | TCCATCATGTACTTCAGCCACTTCGTCGGCTTCTCTGCCAGCAAGCCACGACG | 485 | |
| QY | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 | |
| Db | 486 | CCAGAGCGCGACCAACACCGCGCGCCACCATCGCGTGCACAGGGGGTGGACTTCGCC | 605 | |
| QY | 181 | CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu | 200 | |
| Db | 606 | TGTGATATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTGTCTACATG | 665 | |
| QY | 201 | ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro | 220 | |
| Db | 666 | GTATACACCTTTACTGCAACACAGGAACCGAAGCGTGTTCGCAATGTCCCCGGCT | 725 | |
| QY | 221 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 235 | |
| Db | 726 | GTGGTCAATCGGAGACAAAGCCGCTTTCGGCGAGATACGTC | 770 | |

RESULT 7
AR380469
LOCUS
DEFINITION
Sequence 1014 from patent US 6607879.
ACCESSION
AR380469
VERSION
AR380469.1 GI:40088103
KEYWORDS
Unknown.
ORGANISM
Unclassified.
1 (bases 1 to 1060)
Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
Compositions for the detection of blood cell and immunological
response gene expression
Patent: US 6607879-A 1014 19-AUG-2003;
Incyte Corporation; Palo Alto, CA

| | | | |
|---|---------------------|---------------|------|
| Location/Qualifiers | | | |
| 1..1060 | /organism="unknown" | | |
| /mol_type="genomic DNA" | | | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. NO.: | 9.95e-91 | Length: | 1060 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |
| US-10-804-763-1 (1-235) x AR380469 (1-1060) | | | |

| | | | |
|----|-----|--|-----|
| QY | 1 | MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg | 20 |
| Db | 66 | ATGGCCTTACCAGTACCGCCTTGCTCCGCGCTGGCTTGTCTCCACGCCGACG | 125 |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| Db | 126 | CCGAGCCAGTTCGGGGTTCGGATCGGACCTGGAACTGGCGGAGACAGTGGAG | 185 |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAenProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 186 | CTGAAGTGCAGGTCTGCTCCAAACCGAGTCGGGCTGCTCGTGGCTCTTCCAGCCG | 245 |
| QY | 61 | ArgGlyAlaAlaSerProThrPheLeuLeuLeuSerGlnAsnLysProLysAla | 80 |
| Db | 246 | CGCGGGCGCGCCAGTCCACCTTCTCTATACCTTCCAAACAGCCCAAGGCG | 305 |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyValLeu | 100 |
| Db | 306 | GCGGAGGGCTGACACCCAGCGGTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTC | 365 |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
| Db | 366 | ACCTTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC | 425 |
| QY | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr | 140 |
| Db | 426 | TCCATCATGTACTTCAGCCACTTCGTCGGCTTCTCTGCCAGCAAGCCACGACG | 485 |
| QY | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| Db | 486 | CCAGAGCGCGACCAACACCGCGCGCCACCATCGCGTGCACAGGGGGTGGACTTCGCC | 605 |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla | 180 |
| Db | 546 | CCAGAGCGGTGCGCGCCAGCGGGGGCGAGTGCACACAGGGGGCTGGACTTCGCC | 605 |
| QY | 181 | CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu | 200 |
| Db | 606 | TGTGATATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTGTCTACATG | 665 |
| QY | 201 | ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro | 220 |
| Db | 666 | GTATACACCTTTACTGCAACACAGGAACCGAAGCGTGTTCGCAATGTCCCCGGCT | 725 |
| QY | 221 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 235 |
| Db | 726 | GTGGTCAATCGGAGACAAAGCCGCTTTCGGCGAGATACGTC | 770 |

RESULT 8
HUMATCT8A
LOCUS
DEFINITION
Homo sapiens T-cell surface protein T8 mRNA.
ACCESSION
M12828
VERSION
M12828.1 GI:179145
KEYWORDS
cell surface glycoprotein.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

No

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

Littman,D.R., Thomas,Y., Maddon,P.J., Chess,L. and Axel,R.
The isolation and sequence of the gene encoding T8: a molecule
defining functional classes of T lymphocytes

JOURNAL

Cell 40 (2), 237-246 (1985)

PUBMED

3871356

COMMENT

Original source text: Human peripheral T cell, cDNA to mRNA, clones
pT8.B and pT8.F1.

FEATURES

source

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/mol_type="mRNA"

/db_xref="taxon:9606"

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66..773

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/codon_start=1

/protein_id="AAB04637.1"

/db_xref="GI:179146"

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/note="cell surface glycoprotein T8 signal peptide"

126..770

/product="cell surface glycoprotein T8"

774..1060

ORIGIN

Alignment Scores:

Pred. No.: 9,956-91 Length: 1060

Score: 1247.00 Matches: 235

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x HUMATCT8A (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHieAlaAlaArg 20

Db 66 ATGGCTTACAGTAGCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCCAGG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 126 CCGAGCCAGTTCGGGTGTCGGCGTGGACCTGGAACCTGGCGGAGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 186 CTGAAGTGCAGGTGCTGTCTCCACCGACGTGGGTGCTGTGGCTCTTCCAGCGG 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80

Db 246 CG 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 306 CGCGAGGGGCTGACACCCAGCGGTCTCGGCAAGAGGTTCGGGGACACCTTCGCTC 365

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120

Db 366 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGCGCTGAGC 425

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140

Db 426 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCCAGCGAAGCCACCGACG 485

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 486 CCAGCGCGGACACCAACACCGCGCCACCATCGCTCGCAGCCCTGTCCCTGCGC 545

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180

Db 546 CCAGAGCGGTGCCCGCAGCGCGGGCGGCGCACTGCACACAGGGGGCTGGACTTCGCC 605

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200

Db 606 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACTG 665

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgValCysLysCysProArgPro 220

Db 666 GTTATCACCTTTACTGCACCAACAGGAACGAGACGTGTTCGAAATGTCCTCCGCGCT 725

Qy 221 ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 235

Db 726 GTGTCAATCGGAGACAGCCAGCTTTCGGCGGAGATACGTC 770

RESULT 9

HUMTCXAAA

LOCUS Human T-cell differentiation antigen Leu-2/T8 mRNA, linear PRI 14-JAN-1995

DEFINITION Human T-cell differentiation antigen Leu-2/T8 mRNA, partial cds.

ACCESSION M12824

VERSION M12824.1 GI:339426

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 775)

Sukhatme,V.P., Sizer,K.C., Vollmer,A.C., Hunkapiller,T. and

Parnes,J.R.

The T cell differentiation antigen Leu-2/T8 is homologous to

immunoglobulin and T cell receptor variable regions

Cell 40 (3), 591-597 (1985)

COMMENT 3918796

Original source text: Human, cDNA to mRNA, clone pL2-M.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="2p12"

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/gene="CD8"

1..>1975

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/product="T-cell differentiation antigen Leu-2/T8 mRNA"

88..795

/gene="CD8"

/note="T-cell differentiation antigen Leu-2/T8"

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/protein_id="AAA61133.1"

/db_xref="GI:339427"

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VLLSNPTGCSWLFPQPGAASTPFLYLSQNKPKAAEGLDTQFSGKRLGDTFVLT

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PEACRPAAGAVHTRGLDFACDIYIWAFLAGTCGVLISLVLITLYCNHRRNRVCKCP

RPVVKSGDKPSLSARYV"

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/note="T-cell differentiation antigen Leu-2/T8 signal

peptide"

151..792

/gene="CD8"

/product="T-cell differentiation antigen Leu-2/T8 mature

peptide"

ORIGIN Chromosome 2p12.

Alignment Scores:

Pred. No.: 1.77e-90 Length: 1975
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x HUMTCXAAA (1-1975)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 88 ATGGCCTTACCAAGTACCGCTTGGCTTCTGCGCGCTGGCTTGTCTCCACGCGCGCAGG 147
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 148 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 207
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 208 CTGAAGTGCAGGTGTCTGTCTCAACCGACGTCGGGTGTCTGGTCTCTTCCAGCGG 267
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 268 CGGGGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCG 327
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 328 GCCAGGGGCTGGACACCGCGGTTCGGGCAAGAGGTGGGGGACACCTTCGTCTCTC 387
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 388 ACCCTGAGCGACTTCGGCGGAGAAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 447
QY 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 448 TCCATCATGTACTTACGCCACTTCTGTCGGCTTCTGTCAGCGAAGCCACCGACG 507
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 508 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCTCTGCGC 567
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 568 CCAGAGCGGTGCGCGCAGCGCGGGGCGAGTGCACACGAGGGGGTGGACTTCGCG 627
QY 181 CysAspIleTyrrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 628 TGTGATATCTACATCTGGCGCGCCCTGCGCGGACTTGTGGGTCTCTCTCTGTCTG 687
QY 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgValCysLysCysProArgPro 220
Db 688 GTTATCACCCTTTACTTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTC 747
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
Db 748 GTGGTCAATCGGGAGACAAAGCCAGCCCTTCGGCGAGATACGTC 792

RESULT 10
CQ882010
LOCUS CQ882010 2261 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 2 from Patent WO2004083404.
ACCESSION CQ882010
VERSION CQ882010.1 GI:54034736
KEYWORDS

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Qi, Y., Zhang, X. and Konigsberg, P. J.
AUTHORS Gene therapy vectors having reduced immunogenicity
TITLE Patent: WO 2004083404-A 2 30-SEP-2004;
JOURNAL

See primly to 3000
appl.

Isogenis, Inc. (US)
Location/Qualifiers
1. .2261
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-90 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x CQ882010 (1-2261)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACCAAGTACCGCTTGGCTTCTGCGCGCTGGCTTGTCTCCACGCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGTCTGTCTCAACCGACGTCGGGTGTCTGGTCTCTTCCAGCGG 239
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 300 CGGGGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCAGGGGCTGGACACCGCGGTTCGGGCAAGAGGTGGGGGACACCTTCGTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGGCGGAGAAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 479
QY 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTACGCCACTTCTGTCGGCTTCTCTCTGCGCGCGCTTGAGCAAC 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCTCTGCTG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGGGGTGCGCGCAGCGCGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCG 659
QY 181 CysAspIleTyrrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGGAGCTTGTGGGTCTCTCTCTGTCTG 719
QY 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCTTTACTTGCAACACAGAAACCGAAGACGTGTTTGCAAAATGTC 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
Db 780 GTGGTCAATCGGGAGACAAAGCCAGCCCTTCGGCGAGATACGTC 824

RESULT 11
AX764527
LOCUS AX764527 708 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 44 from Patent WO20102852.
ACCESSION AX764527
VERSION AX764527.1 GI:32258735
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Jakobsen,B.K. and Glick,M.
TITLE Modified CD8 molecule, nucleic acid encoding said molecule, and their therapeutic use
JOURNAL Patent: WO 02102852-A 44 27-DEC-2002;
Avidex Limited (GB)
FEATURES Location/Qualifiers
source 1..708
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
CDS 1..708
/note="unnamed protein product; modified protein"
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/db_xref="GI:32258736"
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ORIGIN
Alignment Scores:
Pred. No.: 1.19e-90 Length: 708
Score: 1244.00 Matches: 234
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 99.8% Indels: 0
DB: 2 Gaps: 0
US-10-804-763-1 (1-235) x AX764527 (1-708)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisaAlaArg 20
Db 1 ATGGCTTTACCAAGTACCGCCCTTGTCTCGCGTGGCGCTTGTCTCCACGCGCCACG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTGGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTCGGGTGTCTGTGCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 CGCGAGGGGCTGGAACCCAGCGGTCTCGGGCAAGAGTGGGGGACACCTTCGTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCGCGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGGCACCTTCGTGGCGGTCTTCCTGCCAGCGAAAGCCACACGAG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CAGCGCGCGCGGACCAACACCGCGGCCACCATCGCGTCCGACGCCCTGTCCCTGGCG 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGCGTCCGCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY 181 CysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTTGTGGGGTCCCTTCTCTGTCACTG 600
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCTTTACTGCAACACGAGACGAGCGTGTTCGAATGTCCCGGCGCT 660
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAAGCCCGAGCTTTCGGCGAGATACGTC 705
RESULT 12
AY039664 1018 bp mRNA linear PRI 17-JUL-2001
LOCUS Homo sapiens mutant CD8 alpha antigen (CD8A) mRNA, complete cds.
DEFINITION
ACCESSION AY039664
VERSION AY039664.1 GI:14861039
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE 1 (bases 1 to 1018)
AUTHORS de la Calle-Martin,O., Hernandez,M., Ordi,J., Casamitjana,N.,
Arostegui,J.I., Caragol,I., Ferrando,M., Labrador,M.,
Rodriguez-Sanchez,J.L. and Espanol,T.
Familial CD8 deficiency due to a mutation in the CD8 alpha gene
J. Clin. Invest. 108 (1), 117-123 (2001)
11435463
REFERENCE 2 (bases 1 to 1018)
AUTHORS Casamitjana,N., Arostegui,J.I. and de la Calle,O.
Direct Submission
TITLE Submitted (12-JUN-2001) Immunohematology, Centre de Transfusio i
Banc de Teixits, Pg. de la Vall d'Hebron 119-129, Barcelona 08035,
Spain
FEATURES Location/Qualifiers
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510
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/note="results in Gly to Ser substitution"
/replace="g"
ORIGIN
Alignment Scores:
Pred. No.: 2.91e-90 Length: 1018
Score: 1241.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 5 Gaps: 0
US-10-804-763-1 (1-235) x AY039664 (1-1018)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisaAlaArg 20

Nothing to suggest

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QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
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QY      101  ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
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QY      121  SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
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QY      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeu 160
Db      600  CCAGCGCCCGGACCCACACACCGCGGCCACCATCGCTGGAGCCCTGTCTCTGCGC 659
QY      161  ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db      660  CCAGAGCGCTGCGCGCCAGCGGGGGCGCAGTGCACACAGAGGGGGCTGGACTTCGCC 719
QY      181  CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db      720  TGTGATATATACATCTGGCGCGCCCTGCGCGGAGCTTGTGGGTCTCTCTCTGTCTG 779
QY      201  ValIleThrLeuTyrcysAsnHisArgAsnArgArgArgValCysLysCysProArgPro 220
Db      780  GTTATACACCTTTACTTGCACACACAGAACCGAAGACGTGTTCGAAATGTCCCCGGC 839
QY      221  ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
Db      840  GTGGTCAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 884

RESULT 13
BC025715
LOCUS
DEFINITION
Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript
variant 1, mRNA (cdna clone MGC:34614 IMAGE:5227906), complete cds.
ACCESSION
BC025715
VERSION
BC025715.1 GI:19344021
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 2150)
Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Strausberg,R.L., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,I., Max,S.I., Wang,J., Hsieh,F.,
Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Shapleton,M., Soares,M.B., Bonaldo,M.F., Casavet,T.L.,
Scheetz,T.E., Brownstein,M.J., Usgin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.C., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Brakesley,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2150)

Strausberg,R.

Direct Submission

Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 49 Row: 0 Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27886641.

FEATURES

Location/Qualifiers

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/clone="MGC:34614 IMAGE:5227906"

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gene

CDS

ORIGIN

Alignment Scores:

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Score: 1238.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.3% Indels: 0
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US-10-804-763-1 (1-235) x BC025715 (1-2150)

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
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Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGAGTGTCTGTCCAAACCGGACGTGGGCTGTCTGTGGCTCTTCCAGCGG 185
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGGCGCGCGCGGCGGACCTTCTCTATACCTTCTCCAAAACAGACCCAGCGG 245
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
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Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
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Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
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Db 666 GTGGTCAATCGGAGACAAGCCAGCCTTTCGGCGGAGATACGTC 710

RESULT 14

CQ843147 CQ843147 3048 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 1794 from Patent EP1440981.
ACCESSION CQ843147
VERSION CQ843147.1 GI:50894934

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.

TITLE

JOURNAL Full-length human cdna
Patent: EP 1440981-A 1794 28-JUL-2004;
Research Association for Biotechnology (JP)

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
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Alignment Scores:
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Score: 1236.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.1% Indels: 0
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US-10-804-763-1 (1-235) x CQ843147 (1-3048)

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Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
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Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 1392 TCCATCATGTACTTCAGCACCTTCTGTCGGGTCTTCTCTGCCAGGAAGCCACACGACG 1451
Qy 141 ProAlaProArgProProThrProAlaProThrileAlaSerGlnProLeuSerLeuArg 160
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Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
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Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
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Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
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RESULT 15

AK124156 AK124156 3048 bp mRNA linear PRI 20-JAN-2006
LOCUS Homo sapiens cDNA FLJ42162 fis, clone THYMU2005303, highly similar
DEFINITION to T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR.

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 29, 2006, 22:39:21 ; Search time 904.723 Seconds

(without alignments)
2716.542 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 36 | 809 | 64.9 | 785 | 13 | ADS19457 |
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ALIGNMENTS

RESULT 1
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ID AAX80967 standard; cDNA; 708 BP.
AC AAX80967;
XX
XX
DT 18-AUG-1999 (first entry)
XX
DE Human CD8 alpha protein encoding cDNA.
XX

KW T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;
KW corticosteroid; human; CD8 alpha protein; ss.
XX
OS Homo sapiens.
PN WO921576-A1.
XX
PD 06-MAY-1999.
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PF 28-OCT-1998; 98WO-GB003235.
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PR 28-OCT-1997; 97GB-00022779.
XX

Submit form
No

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XX DR WPI; 1999-385058/32.
XX DR P-PSDB; AAY21688.
XX PT Inhibiting activity of T cells against target cells useful for treating
XX PT autoimmune diseases and allergy.
XX PS Disclosure; Fig 1A; 79pp; English.
XX SS
XX CC The invention describes a method for inhibiting activity of T lymphocytes
XX CC against a target cell by treating the cell with a soluble form of a CD8
XX CC molecule. The method is used as immunosuppressive therapy, e.g. in
XX CC patients undergoing transplantation, but also for treating autoimmune
XX CC diseases and allergy, e.g. exacerbation of asthma caused by viral
XX CC infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
XX CC vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment
XX CC with CD8 protein provides more selective immunosuppression than use of
XX CC corticosteroids. The present sequence represents a cDNA encoding a human
XX CC CD8 alpha protein
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x AXH0967 (1-708)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 1 ATGGCTTTACAGTGCACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGACG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 61 CCGAGCCAGTTCGGGGTTCGGCGTGGATCGGACCTGGAACTGGGGGAGACAGTGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 121 CTGAAGTCCAGGTCGTCTGCCAACCGAGCTCGGGCTGCTGTGCTCTTCAGCG 180
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DB 181 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTTCTCCAAACAAAGCCCAAGGCG 240
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DB 241 GCCGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
DB 301 ACCCTGAGCGACTTCGGCGGAGAACGAGGGCTACTATTCTGCTCGGCTCTGAGCAAC 360
QY 121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 361 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCGAAGCCACACGACG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 421 CCAGCGCGCGCACCAACACCGCGGCCACCATCGGTGTCGACGCCCTGTCTCCCTGGGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 481 CCAGAGGGGTGCCGCGCCAGCGCGGGCGCGAGTGCACACAGGGGGCTGGACTTCGCC 540
QY 181 CysAspIleTyTrpIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
DB 541 TGTGATATCTACATCTGGGCGGCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCACTG 600
QY 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220

Db 601 GTTATCACCTTTACTGCAACCCACAGGAACGAGAGCGTGTGCAATGTCCTCCGCGCT 660
QY 221 ValVallySerGlyAspLysProSerLeuSerAlaArgTyTrVal 235
DB 661 GTGGTCAAAATCGGAGACACAGCCAGCCTTTTCGGGGAGATAGCTC 705

RESULT 2
ABZ69260
ID ABZ69260 standard; DNA; 708 BP.
XX AC ABZ69260;
XX DT 11-AUG-2003 (first entry)
XX DE Human CD8alpha chain coding sequence.
XX KW Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;
XX KW antiallergic; cytotoxic T cell response; inhibitor; gene; ds.
XX OS Homo sapiens.
XX PN WO2002102852-A2.
XX PD 27-DEC-2002.
XX PF 14-JUN-2002; 2002WO-GB002743.
XX PR 14-JUN-2001; 2001GB-00014533.
XX PA (AVID-) AVIDEX LTD.
XX PI Jakobsen BK, Glick M;
XX DR WPI; 2003-167488/16.
XX DR P-PSDB; AAO19807.
XX PT New modified CD8 molecule having enhanced binding to major
XX PT histocompatibility complex, and having a Serine53 of at least one CD
XX PT alpha chain is mutated to another amino acid, useful for treating e.g.
XX PS graft rejection or hypersensitivity.
XX PS Disclosure; Fig 1A; 60pp; English.
XX CC The present invention provides modified human CD8 molecules whose binding
XX CC to major histocompatibility complex (MHC) is enhanced compared to wild
XX CC type CD8. The modified CD8 molecule or a corresponding nucleic acid is
XX CC useful in medicine, particularly in manufacturing a medicament for
XX CC modulating CD8+ T cell response. The modified CD8 proteins and nucleic
XX CC acids encoding such proteins are useful in immunosuppressive therapy,
XX CC particularly as inhibitors of cytotoxic T cell responses, and for
XX CC treating autoimmune disorders, hypersensitivity (e.g. allergic reaction),
XX CC graft versus host disease, or graft rejection. The present sequence is a
XX CC CD8 coding sequence
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-804-763-1 (1-235) x ABZ69260 (1-708)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 1 ATGGCTTTACAGTGCACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGACG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
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Db 61 CCGAGCCAGTTCGGGTGCTGGCGCTGGATCGGACCTGGAACTGGGGGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCAGGTGCTGTCTCAACCCGACGTCTGGGTCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCGGAGGGCTGACACCCAGCGTCTCGGCGAGAGGTGGGGACACCTTCGTCCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluTyrlTyrlPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCATCATGATCTTACGCGACTTCGTCGGCTCTTCTGCGAGGAGCCACCGAGCG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGGCGCGCGACCAACACCGCGCGCCACCATCGCTCGGAGCCCTGTCTCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGCGTCCGCGCGCGCGCGCGCGCGCGAGTGCACACGAGGGGCTGGACTTCGCC 540
QY 181 CysAspIleTyrlleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGGCGCGCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCTACATG 600
QY 201 ValIleThrLeuTyrlCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCTTTACTGCAACACAGAAACCGAAGACGTGTTCGAAATGTCCCGGCT 660
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrlVal 235
Db 661 GTGGTCAATCGGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 705
```

RESULT 3

ADS92817

ID ADS92817 standard; cDNA; 708 BP.

XX AC

XX ADS92817;

XX DT

XX 16-DEC-2004 (first entry)

XX DE

XX Nucleotide sequence of a CD8 alpha-chain protein.

XX KW

XX immune response; cell-specific antigen; alloantigen; CD8;

XX CD8 alpha-chain; cellular immune response; humoral immune response;

XX KW transplant allograft; graft-versus-host disease; recipient; gene; ss.

XX OS

XX Homo sapiens.

XX FH

XX Key Location/Qualifiers

XX CDS

XX 1..708

XX /*tag= b

XX /*product= "CD8 alpha-chain"

XX sig_peptide

XX 1..63

XX /*tag= a

XX FT

XX WO2004083244-A2.

XX PN

XX 30-SEP-2004.

XX PD

XX 19-MAR-2004; 2004WO-05008574.

XX PF

XX 19-MAR-2003; 2003US-0456378P.

XX PR

XX XX

PA (ISOG-) ISOGENIS INC.

XX

PI Qi Y, Zhang X, Konigsberg PJ;

XX

DR WPI: 2004-691022/67.

XX

XX P-PSDB; ADS92816.

XX

Specifically inhibiting host immune responses to alloantigens, useful for e.g. treating graft-versus-host disease, comprises contacting a target cell expressing the antigen with an expression vector encoding a CD8 polypeptide.

XX

PS Disclosure; Fig 1; 98pp; English.

XX

The specification describes a method for specifically inhibiting a host immune response to target cell-specific antigens (e.g. alloantigens). The method comprises contacting a target cell expressing the antigen with an expression vector encoding a CD8 polypeptide comprising the CD8 alpha-chain, where the CD8 polypeptide is expressed by the target cell and where the host immune response against the target cell is specifically inhibited. The method of the invention is useful for specifically inhibiting both cellular and humoral immune responses to alloantigens, thus finding use in extending the survival of transplant allografts and in treating graft-versus-host disease in transplant recipients. The present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha-chain may be used in the method of the invention.

XX

SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 6,978-93 | Length: | 708 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-804-763-1 (1-235) x ADS92817 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 1 ATGGCTTACAGTACCGCTTGTCTCTGCGTGGCTTGTCTCTCCAGCCGCGAGG 60

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 61 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGACCTGGCGAGACAGTGGAG 120

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 121 CTGAAGTGCAGGTGCTGTCTCAACCCGAGCTGGGCTGTCTGTGGCTCTTCCAGCCG 180

QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAla 80

Db 181 CGCGGGCGCGCGCGCGAGTCCACCTTCTCTCTATACCTCTCCAAACCAAGCCCAAGGCG 240

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 241 GCGGAGGGCTGACACCCAGCGGTCTCGGCGAGAGGTGGGGACACCTTCGTCCTC 300

QY 101 ThrLeuSerAspPheArgGluAsnGluTyrlTyrlPheCysSerAlaLeuSerAsn 120

Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTCGGCCCTGAGCAAC 360

QY 121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140

Db 361 TCATCATGATCTTACGCGACTTCGTCGGCTCTTCTCTCCAGCGAGCCACCGAGCG 420

QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 421 CCAGGCGCGCGACCAACACCGGGCGCCACCATCGCTCGGAGCCCTGTCTCTGCGC 480

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180

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Db 481 CCAGAGGGCTCCGGCCAGCGGGGGGGCCAGTGCACAGAGGGGCTGGACTTCGCC 540
Qy 181 CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCCCTTGGCCGGACTTGTGGGTCCTTCTCTGTCACTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCTTTACTGCAACACAGGAAACGAGACGTGTTGCAATGTCCCGGCT 660
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 705

RESULT 4

ADS19462

ID ADS19462 standard; DNA; 708 BP.

XX AC

ADS19462;

XX DT

16-DEC-2004 (first entry)

XX DE

Coding sequence DNA of the human CD8 alpha chain mRNA.

XX KW

gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
humoral immune response; immunosuppressive.

XX OS

Homo sapiens.

XX FH

Key Location/Qualifiers

XX FT

1..708

XX FT

/*tag= a

XX FT

/product= "CD8 alpha chain protein"

XX PN

WO2004083404-A2.

XX PD

30-SEP-2004.

XX PF

19-MAR-2004; 2004WO-US008567.

XX PR

19-MAR-2003; 2003US-0456378P.

XX PA

(ISOG-) ISOGENIS INC.

XX QI

Yi Y, Zhang X, Konigsberg PJ;

XX PI

WPI; 2004-691049/67.

XX DR

P-P5DB; ADS19436.

XX DR

New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain

XX PT

operably linked to a nucleic acid encoding a transmembrane polypeptide,

XX PT

useful for inhibiting cellular and humoral components of the host immune

XX PT

responses.

XX PS

Disclosure; Fig 2a; 94pp; English.

XX CC

This invention relates to novel gene therapy vectors with reduced

XX CC

immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8

XX CC

alpha chain operably linked to nucleic acid encoding a transmembrane

XX CC

polypeptide and a second nucleic acid representing the therapeutic gene

XX CC

of interest (for example ornithine carbamoyl transferase or beta

XX CC

glucosidase), whereby transcriptional and translational control elements

XX CC

direct expression thereof. The present invention describes a method to

SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS19462 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20

Db 1 ATGGCCTTACCAGTGCAGCGCTTCTCTCGCGCTGGCCTTGTCTCTCCAGCCCGCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 61 CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 121 CTGAAGTCCAGGTGCTGTCTCAACCCGAGCTCGGCTGTCTGTGTCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTCTATACCTTCTCCAAACCAAGCCCAAGCGG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 241 GCCAGGGGCTGGACACCCAGCGTTCTCGGGCAAGAGTTGGGGGACACCTTCTCTCTC 300

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGTCTCGGCCCTGAGCAAC 360

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140

Db 361 TCCATCATGTACTTTCAGCCACTTCTGTGCGGTCTTCTCTGCCAGCAAGCCACACGACG 420

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 421 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTCTCTCTGCGC 480

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180

Db 481 CCAGAGGCGTCCGCGCAGCGCGGGGCGCAGTGCACACGAGGGGCTGGACTTCGCC 540

Qy 181 CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200

Db 541 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTCTGTCACTG 600

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220

Db 601 GTTATCACCTTTTACTGCAACACAGGAAACGAGACGTGTTTGCAATGTCTCCCGGCT 660

Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235

Db 661 GTGGTCAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 705

RESULT 5

ADV42461

ID ADV42461 standard; cDNA; 708 BP.

XX AC

ADV42461;

XX DT

10-MAR-2005 (first entry)

XX DE

Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 89.

XX KW

microarray; psychoneuroendocrinimmune; chronic fatigue;

XX KW

non-insulin dependent diabetes; allergy; immune disorder; inflammation;

XX KW

cancer; neoplasm; infection; expressed sequence tag; ss.

No

XX Homo sapiens.
OS WO2004108899-A2.
PN 16-DEC-2004.
PD 04-JUN-2004; 2004WO-US017686.
PF 04-JUN-2003; 2003US-0475915P.
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Nicholson A, Vernon SD;
PI WPI; 2005-031682/03.
DR New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX Claim 1; SEQ ID NO 89; 254pp; English.
XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specification mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-804-763-1 (1-235) x ADV42461 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACCAAGTACCGCTTGTCTCTCGCGCTGGCTTCTCTCAGCCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGCTCTGTGTCACCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 181 CG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCGCGGTTCCTCGGCGAGAGGTTGGGGGACACCTTCCTCCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAAC 360
Qy 121 SerileMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGCCACTTCGTGGCGGCTTCTTCTGCCAGCGAAGCCACCCAGCAG 420

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGCGTGCAGCCCTGTCCCTGCCG 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGGGTGCCG 540
Qy 181 CysAspIleTyTrpIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCGCTTGGCGGAGACTTGTGGGGTCTCTTCTGTCTGCTG 600
Qy 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCTTTACTGCAACCCACAGAACCGAGACGCTGTTGCAAAATGTCCCGGCGCT 660
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyTrpVal 235
Db 661 GTGGTCAATCGGGAGACAGCCCGCTTTCGGCGAGATACGTC 705

RESULT 6
AEF68357
ID AEF68357 standard; cDNA; 708 BP.
XX AC AEF68357;
XX DT 06-APR-2006 (first entry)
XX DE Human CD8 alpha chain cDNA.
XX KW immune inhibition; CD8; spinal cord injury; neuroprotective; vulnary;
KW autoimmune disease; immunosuppressive; immune disorder; diabetes;
KW antidiabetic; endocrine disease; gastrointestinal disease;
KW metabolic disorder; uveitis; antiinflammatory; ophthalmological;
KW inflammation; cirrhosis; hepatotropic; gastrointestinal disease;
KW neurodegenerative disease; neuroprotective; neurological disease;
KW osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease;
KW obesity; anorectic; nutritional disorder; ss; gene.
XX Homo sapiens.
Key Location/Qualifiers
FT 1..708
FT /*tag= b
FT /product= "CD8 alpha chain"
FT /transl_except= (pos:67..69,aa:Gly)
FT /transl_except= (pos:130..132,aa:Gly)
FT /transl_except= (pos:175..177,aa:Gly)
FT /transl_except= (pos:223..225,aa:Gly)
FT /transl_except= (pos:259..261,aa:Gly)
FT /transl_except= (pos:463..465,aa:Gly)
FT sig_peptide 1..63 /*tag= a
FT mat_peptide 64..705 /*tag= c
FT /*tag= c
FT /product= "Mature CD8 alpha chain"
XX WO2006012416-A2.
XX 02-FEB-2006.
XX 20-JUL-2005; 2005WO-US025878.
XX 20-JUL-2004; 2004US-0589707P.
XX 29-SEP-2004; 2004US-0614529P.
XX (ISOG-) ISOGENIS INC.
XX Qi Y, Staerz UD;
XX WPI; 2006-125925/13.
XX P-PSDB; AEF68356.

late
hoo

PT New composition comprising CD8 polypeptide and autoantigen protein,
PT useful for preventing or treating autoimmune disease, diabetes,
PT neurodegenerative diseases, osteoarthritis.

XX
PS Disclosure; Fig 1A; 85pp; English.

XX The invention relates to a therapeutic composition for inhibiting an
CC autoreactive T cell response, comprising an expression vector encoding a
CC CD8 polypeptide and an autoantigen protein or its fragment, or at least
CC one epitope of an autoantigen associated with the autoreactive T cell
CC response. Also described are: (1) a polynucleotide comprising a first
CC nucleic acid sequence encoding a CD8 polypeptide, a second nucleic acid
CC sequence encoding at least one epitope of an autoantigen associated with
CC an autoreactive T cell response, and control sequences operably linked
CC with the first and second nucleic acids for expression in a target cell;
CC (2) a method for inhibiting an autoimmune response to a target antigen;
CC and (3) a method of preventing the development of or for treating an
CC autoimmune disease in a host. The composition and methods are useful for
CC inhibiting an autoimmune response to a target antigen, and for preventing
CC the development of or for treating autoimmune disease, diabetes, uveitis,
CC cirrhosis, neurodegenerative diseases (e.g. Alzheimer's disease,
CC Huntington's disease, or Parkinson's disease), osteoarthritis, obesity,
CC or spinal cord injury. The present sequence represents human CD8 alpha
CC chain cDNA.

XX
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6, 97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 15 Gaps: 0

US-10-804-763-1 (1-235) x ABP68357 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACCGATGACCGCTTGTCTCGCGCTGGCTGTCTCCAGCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTTCGCGCTGGATCGACCTGGACCTGGCGGACAGCTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGTCTCCACCGAGCTCGGCTGTCTGTCTCTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCGCTCCACCTTCCTCTATACCTCTCCAAACCAAGCCCAAGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCGCGGTTCGCGCAAGAGTGGGGACACCTTCGCTCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGACGACTTCGCGCGAGAACGAGGGCTACTATTCTGCTCGGCTTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGGCACCTTCGTCGGGTCTTCCTGCCAGCGAAGCCACCAAGCG 420
Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGGCCACCATCGCGTCCGACCCCTGTCTCTCGCG 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGCGAGTGACACAGGGGGGTGGACTTCGCC 540

Qy 181 CysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCATCATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTGTCACTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 501 GTTATCACCTTTACTGCAACCAACGAGACGTTGTTGCAATGTCTCCCGGCGCT 660
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAAGCCCGAGCTTTTCGGCGGATACGTC 705

RESULT 7

AAQ57986

ID AAQ57986 standard; DNA; 1060 BP.

XX

AC AAQ57986;

XX

DT 25-MAR-2003 (revised)

DT 20-AUG-1994 (first entry)

XX

XX Genomic sequence of human CD8.

DE

KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;

KW fusion protein; CD8; fusion protein; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 66..773

FT /*tag= a

XX

PN EP585943-A2.

XX

PD 09-MAR-1994.

XX

XX 03-SEP-1993; 93EP-00114153.

XX

PR 04-SEP-1992; 92US-00940605.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Aruffo A, Hollenbaugh D, Ledbetter JA;

XX

DR WPI; 1994-076264/10.

XX

DR P-PSDB; AAR59550.

XX

PT New nucleic acid encoding human gp39 T cell antigen - which is a ligand

PT for the CD40 receptor, causing proliferation and differentiation of B

PT cells and some cancer cells.

PS

PS Disclosure; Fig 9; 39pp; English.

XX

CC The complete nucleic acid sequence of human gp39 (hgp39) protein
CC (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in
CC AAQ57984 and AAR49548 respectively and contd. in plasmid CD8-hgp39,
CC deposited with the ATCC as E. coli, CD8 MC1061/p3-hgp39 and assigned
CC accession No. 69050. The human T cell antigen gp39 is a ligand for the
CC CD40 receptor. Soluble gp39 may be produced using the expression vector
CC CD8-gp39. Chimeric genes may be constructed by fusing sequences encoding
CC the extracellular domains of gp39 and CD8, pref. murine or human CD8
CC protein, plasmid p3-shgp39 encoding the fusion protein of the
CC extracellular domains from gp39 and CD8 is deposited in E.coli as ATCC
CC 69049. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,14e-92 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

Handwritten: Citrus fruit

Db 606 TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCTGTCACTG 665
Qy 201 Val1leThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGAACCGAGACGTGTTGCNAATGTCCCGGCT 725
Qy 221 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAATCGGAGACAGCCAGCCTTTTCGGCGAGATACGTC 770

RESULT 9

AD131688

ID AD131688 standard; cDNA; 1060 BP.

XX AC

XX AD131688;

XX 17-JUN-2004 (first entry)

XX DE Human cDNA #1014.

XX Human; gene; ss; immunological response; immunopathological condition;
XX Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
XX irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX osteopathic; antiarthritic; antirheumatic; cytostatic.

XX OS Homo sapiens.

XX XX

XX US6607879-B1.

XX PN 19-AUG-2003.

XX PD 09-FEB-1998; 98US-00023655.

XX PF 09-FEB-1998; 98US-00023655.

XX PR (INCY-) INCYTE CORP.

XX PA Cocks BG, Stuart SG, Seilhamer JJ;

XX PI WPI; 2003-895307/82.

XX DR

XX XX

XX A composition comprising a plurality of cDNAs, useful for detecting

XX altered expression of genes in an immunological response or for

XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma

XX or osteoarthritis.

XX PS Claim 1; SEQ ID NO 1014; 50pp; English.

XX XX

XX The invention relates to a composition comprising a plurality of cDNAs
XX for detecting the altered expression of genes in an immunological
XX response. The invention also relates to a method of diagnosing or
XX monitoring the treatment of an immunopathological condition in a sample,
XX comprising obtaining nucleic acids from a sample, contacting the nucleic
XX acids of the sample with an array comprising the plurality of cDNAs under
XX conditions to form one or more hybridisation complexes, detecting the
XX hybridisation complexes and comparing the levels of the detected
XX hybridisation complexes with the level of hybridisation complexes
XX detected in a non-diseased sample, where an altered level of the detected
XX hybridisation complexes correlates with the presence of an
XX immunopathological condition. Also disclosed are an expression profile
XX comprising a microarray and a plurality of detectable complexes and a
XX method for identifying a plurality of polynucleotide probes. The cDNAs
XX are useful as hybridisable array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray can be used in
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX identifying agents for the treatment of the diseases. The microarray may
XX also be used in drug discovery and development, toxicological and
XX carcinogenicity studies, forensics or pharmacogenomics. The composition
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or

CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.14e-92 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservativeness: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-804-763-1 (1-235) x ADI31688 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCCTTACAGTGACCGCCTTGTCTCTGCCGTGGCTTGTCTCCAGCGCCGAGG 125
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTGGCGCTGGTACCGACCTGGAACCTGGGCGGACAGTGGAG 185
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGTCTCAACCCGACGTGGGCTGTCTGTCTCTTCCAGCGG 245
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCGCGCTTCTCTCTATACCTTCTCCAAAACAGCCCAAGGGG 305
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCGAGGGGTGGACACCCAGCGGTCTCTCGGGCAAGAGTTGGGGGACACCTTCTCTC 365
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGCGACTTCCGCGGAGAGACGAGGGCTACTATTTCTGCTCGGCTGTGAGCAAC 425
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTACGCCACTTGTGCGCGGTCTCTCTCCAGCGAAGCCACACGAGG 485
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGGACCAACCAACACCGCGGCCACCATCGCGTCCGAGCCCTGTCTCTGCGC 545
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGGCGTCCCGGCCAGCGCGGGGGCGAGTGCACACGAGGGGGCTGACTTCGCGC 605
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCATCATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTCTTCTCTGTCTG 665
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTTGCNAATGTCCCGGCT 725
Qy 221 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAATCGGAGACAGCCAGCCTTTTCGGCGAGATACGTC 770

RESULT 10

ADS83755

ID ADS83755 standard; cDNA; 1060 BP.

XX AC

XX ADS83755;

XX DT 11-AUG-2005 (first entry)

XX XX

No

DE Human lymph node cDNA #1014.
XX ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
OS Homo sapiens.
XX
XX US2004077003-A1.
XX
XX 22-APR-2004.
XX
XX 14-AUG-2003; 2003US-00641643.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX
XX WPI; 2004-387937/36.
XX
XX New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
XX Claim 15; SEQ ID NO 1014; 16pp; English.
XX
XX The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=2004007003).
XX
XX Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.14e-92 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS83755 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 66 ATGGGCTTACCAAGTACCGCCCTTGCTCCGCGCTGGCTTGTCTCCACGCCGCGCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 126 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGAGCTGGAACTGGCGGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTGCAGGTGCTGTGCTCCAAACCGACGTCGGGTGCTCGTGGCTCTTCCAGCGG 245
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 246 CGCGGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

DB 306 GCCGAGGGGCTGCACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCGTCTC 365
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 366 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCGTCTGGCCCTTGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
DB 426 TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCCTGCCAGGAGCCACACGACG 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCAGCGCGCGGACCAACACCGCGCCACCATCGCTCGCAGCCCTGTCCCTGCGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 546 CCAGAGGGGTGCG 605
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
DB 606 TGTGATATCTACATCTGGGCGCCTTGCGCGGACTTGTGGGGTCTTCTCTGTCTACTG 665
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
DB 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTTGCAATGTCCCGGCGCT 725
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
DB 726 GTGGTCAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 11
ADF90782
ID ADF90782 standard; DNA; 2123 BP.
XX ADF90782;
XX 26-FEB-2004 (first entry)
XX Human hepatic-fibrosis disease marker SEQ ID 244.
XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
KW hepatic carcinoma; human; ds.
XX Homo sapiens.
XX JP2003259877-A.
XX 16-SEP-2003.
XX 11-MAR-2002; 2002JP-00065013.
XX 11-MAR-2002; 2002JP-00065013.
XX (SUMU) SUMITOMO SEIYAKU KK.
XX WPI; 2003-821598/77.
XX Hepatic fibrosis disease markers comprising polynucleotides or
PT antibodies, useful for improved diagnosis, screening and developing drugs
PT to treat hepatitis, to control cirrhosis and carcinoma.
XX Claim 1; SEQ ID NO 244; 313pp; Japanese.
XX The present invention relates to hepatic-fibrosis disease markers
CC (ADF90339-ADF90871) and related proteins (ADF90872-ADF90917). The
CC sequences are useful for detecting and treating hepatic fibrosis caused
CC by alcohol consumption, virus infection, etc., and the associated chronic
CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
CC precision), so more suitable treatments can be developed and given.
XX Sequence 2123 BP; 508 A; 586 C; 528 G; 501 T; 0 U; 0 Other;
SQ

Alignment Scores: 2.69e-92 Length: 2123
Pred. No.: 1247.00 Matches: 235
Score: 1247.00
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x ADF90782 (1-2123)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 81 ATGGCCCTTACAGTGACCGCTTGTCTCGCTGGCTTGTCTCCAGCCGCGCAGG 140

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 141 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 200

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 201 CTGAAGTCCAGGTGCTGCTCCAAACCGACGTCGGGCTGCTGGCTCTCCAGCGC 260

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 261 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAAGCCCAAGCGC 320

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 321 GCCAGGGGCTGGACACCCAGCGTTCGCGGCAAGAGTTGGGGACACCTTGTCTCTC 380

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 381 ACCCTGAGCGACTTCGGCGAGAGAAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 440

Qy 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 441 TCCATCATGTACTTCAGCCACTTGTGCGCGTCTTCTGCGGAGGAAAGCCACACGACG 500

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 501 CCAGCGCGCGACACACACCGCGCGCCACCATCGGCTCGACGCCCTGTCTCTGCGC 560

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 561 CCAGAGGCGTCCGCGCCAGCGCGCGCGCGCGAGTGCACACGAGGGGCTGGACTTCGCC 620

Qy 181 CysAspIleTyrrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 621 TGTGATATCTACATCTGGGCGCGCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTG 680

Qy 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 681 GTTATCACCTTTACTGCAACACAGAAACCGAAGACGTGTTGCAATGTCCCGGCT 740

Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
Db 741 GTGGTCAATCGGAGAGCAAGCCAGCTTTTCGGCGAGATACGTC 785

RESULT 12

ADP10406

ID ADP10406 standard; DNA; 2261 BP.

XX AC ADP10406;

XX DT 12-AUG-2004 (first entry)

XX DE Reference mRNA sequences for marker probe #83.

XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;

XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

XX XX Homo sapiens.

OS

XX WO2004042346-A2.
XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX Claim 80; SEQ ID NO 415; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
XX and monitoring of allograft rejection and other disorders.
XX Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.91e-92 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-10-804-763-1 (1-235) x ADP10406 (1-2261)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACAGTGACCGCTTGTCTCGCTGGCTTGTCTCCAGCCGCGCAGG 179

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 239

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTGCAACCCGACGTCGGGCTGCTGGCTCTTCCAGCGC 299

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAAGCCCAAGCGC 359

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGACACCTTGTCTCTC 419

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 120

Db 420 ACCCTGAGGACCTTCGCCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGACTTTCAGCCACTTCGTGGCGGTCTTCTGCCAGGAGGCCACGACG 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGGCGCGGACCCACCAACCGCGGCCACCATCGCTGCGAGGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGCTGCGGCGACGCGGGGGGGCGAGTGCACACAGAGGGGTGACTTCGCC 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCATCATCTGGCGGCCCTTGGCGGGGACTTGTGGGTCTCTCTGTCTAC 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCCTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCCGCCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 824

RESULT 13

ADS92791

ID ADS92791 standard; cDNA; 2261 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

CC chain, where the CD8 polypeptide is expressed by the target cell and where the host immune response against the target cell is specifically inhibited. The method of the invention is useful for specifically inhibiting both cellular and humoral immune responses to alloantigens, and thus finding use in extending the survival of transplant recipients and in treating graft-versus-host disease in transplant recipients. The present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha chain may be used in the method of the invention.

XX SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,91e-92 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS92791 (1-2261)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACCAGTACCGCCTTGTCTCTGCGCGCTGTCTCTCCAGCCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTGCGCGCTGGATCGGACCTCGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGCTGCTGCCAACCGACGTCGGGCTGTCTGCGGTCTCTCCAGCCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyValAspThrPheValLeu 100
Db 360 GCCGAGGGGTGGACACCGCGGTCTCGGCGAGAGGTTGGGGGACACCTTCGTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGACTTTCAGCCACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGGCGCGGACCCACCAACCGCGGCCACCATCGCTGCGAGGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGGGGTGCGGCG 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCATCATCTGGCGGCCCTTGGCGGGGACTTGTGGGTCTCTCTGTCTAC 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCCTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCCGCCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 824

RESULT 14
ADS19437
ID ADS19437 standard; DNA; 2261 BP.
XX

Na

AC ADS19437;
XX 16-DEC-2004 (first entry)
XX DNA of the human CD8 alpha chain mRNA.
XX gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
XX humoral immune response; immunosuppressive.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 120..827
XX /*tag= a
XX /product= "CD8 alpha chain protein"
XX WO2004083404-A2.
XX 30-SEP-2004.
XX 19-MAR-2004; 2004WO-US008567.
XX 19-MAR-2003; 2003US-0456378P.
XX (ISOG-) ISOGENIS INC.
XX Qi Y, Zhang X, Konigsberg FJ;
XX WPI; 2004-691049/67.
XX P-PSDB; ADS19436.
XX New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
XX operably linked to a nucleic acid encoding a transmembrane polypeptide,
XX useful for inhibiting cellular and humoral components of the host immune
XX responses.
XX Disclosure; Fig 1; 94pp; English.
XX This invention relates to novel gene therapy vectors with reduced
XX immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
XX alpha chain operably linked to nucleic acid encoding a transmembrane
XX polypeptide and a second nucleic acid representing the therapeutic gene
XX of interest (for example ornithine carbamoyl transferase or beta
XX glucosidase), whereby transcriptional and translational control elements
XX direct expression thereof. The present invention describes a method to
XX reduce an immune response against antigens derived from a gene therapy
XX delivery system i.e. improving the expression of a therapeutic transgene
XX in a host and improving viral expression vectors with reduced
XX immunogenicity. Accordingly, these compositions are useful for inhibiting
XX both the cellular and humoral components of the host immune responses
XX against expression vectors and target cells transfected with the vectors.
XX As such, they exhibit immunosuppressive activity. This polynucleotide is
XX the DNA sequence of the human CD8 alpha chain mRNA of the invention.
XX SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,91e-92 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS19437 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACAGTGACCGCCTTGCTCTCGCGTGGCCTTGCTGCTCCAGCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTGTCGGCGTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 239

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGTGTCCAAACCCGACGTCGGGCTGCTGCTGCTCTTCCAGCGG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGCCCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACCAAGCCCAAGCG 359
Qy 81 AlaGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGCTTCTCGGGCAAGAGTTGGGGGACACCTTGTCTCTC 419
Qy 101 ThrLeuSerAspPheArgArgGluAsnGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCCGCGGAGAGACGAGGGCTACTATTTCTGCTCGGGCTTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTTCAGCCACTTCTGTCGGGTCTTCTTCCGAGGAAAGCCCAACAGAG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCCACACACCGCGGCCACCACTCGCTCGAGGCCCTGTCTCTGCTGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGGTGCG 659
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 660 TGTATATATCATCTCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGCTGCTG 719
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCTTTACTGCAACCCACACGAGAACCGAAGCGTGTTCGAAATGTCCTCCGCG 779
Qy 221 ValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGTGCTCAATCGGAGACAAGCCAGCGCTTTCGGCGAGATACGTC 824

RESULT 15
ADM86779
ID ADM86779 standard; DNA; 2261 BP.
XX
XX ADM86779;
XX AC
XX 07-APR-2005 (first entry)
XX DE Human CD8 gene.
XX XX
XX XX protein interaction; fusion protein; ss; PCR; primer.
XX XX
XX XX Homo sapiens.
XX OS
XX WO2005007822-A2.
XX FN
XX 27-JAN-2005.
XX PD
XX 09-JUL-2004; 2004WO-US021887.
XX PF
XX 09-JUL-2003; 2003US-0485988P.
XX PR 15-OCT-2003; 2003US-0511918P.
XX PR 27-APR-2004; 2004US-0566113P.
XX XX
XX (SENT-) SENTIGEN BIOSCIENCES INC.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Lee KJ, Axel R, Strapps W, Barnea G;
XX WPI; 2005-102091/11.
XX DR
XX Determining protein/protein interaction modulator comprises contacting

PT the compound to a cell transformed or transfected with G-protein coupled
XX receptor and arrestin.

Example 29; SEQ ID NO 99; 133pp; English.

CC The invention relates to a novel method for determining if a test-
CC compound modulates a specific protein/protein interaction or protein
CC interactions of interest. The method comprises contacting the compound to
CC a cell or samples of cells, each of which has been transformed or
CC transfected with a nucleic acid molecule. The invention further
CC comprises: a recombinant cell, transformed or transfected with any of the
CC nucleic acid molecules; an isolated nucleic acid molecule comprising, in
CC 5' to 3' order, any of the nucleotide sequences described; an expression
CC vector comprising the isolated nucleic acid molecule of above, operably
CC linked to a promoter; a fusion protein produced by expression of the
CC isolated nucleic acid molecule of above; and a test kit, useful for
CC determining if a test compound modulates a specific protein/protein
CC interaction of interest. The methods, nucleic acid molecules, and kit are
CC useful for determining if a test-compound modulates a specific
CC protein/protein interaction or protein interactions of interest. This
CC polynucleotide sequence represents the human CD8 gene used in the method
CC of the invention.

XX
SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 2,91e-92 | Length: | 2261 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-10-804-763-1 (1-235) x ADW86779 (1-2261)

| | | | |
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| QY | 1 | MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg | 20 |
| DB | 120 | ATGGCCTTACCAGTACCGCCTTGCTCTCGCGTGGCCTTGCTGCCAGCGCCAGG | 179 |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| DB | 180 | CGAGCCAGTTCGGGGTGTGGCGGTGGATCGGACCTGGAACTGGGGGAGACATGGGAG | 239 |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| DB | 240 | CTGAAGTGCCAGGTGCTGTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG | 299 |
| QY | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
| DB | 300 | CGCGCGCGCGCGCCAGTCCACCTTCCTCTATACCTTCCCAAAACAAGCCCAAGGCG | 359 |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
| DB | 360 | GCCGAGGGGGCTGGACCCAGCGGTTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC | 419 |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
| DB | 420 | ACCTTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC | 479 |
| QY | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr | 140 |
| DB | 480 | TCCATCATGTACTTCAGGCACCTTCGTGCGGTCTTCCTGCCAGCGAAAGCCACCACG | 539 |
| QY | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| DB | 540 | CCAGCGCGCGGACACCAACACCGCGCGCCACCATCGCGTGGCAGCCCTGTCCCTGCGC | 599 |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla | 180 |
| DB | 600 | CCAGAGGCGTCCCGGCCAGCGGGGGGGGCGAGTGCACACGAGGGGGCTGGACTTCGCC | 659 |
| QY | 181 | CysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu | 200 |

| | | | |
|----|-----|--|-----|
| DB | 660 | TGTGATATCTACATCTGGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTTCTCTGTCACTG | 719 |
| QY | 201 | ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro | 220 |
| DB | 720 | GTTATCACCCCTTTACTGCAACCCACAGGAACCCGAAACGTTGTGCAAAATGTCCCCGCGCT | 779 |
| QY | 221 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 235 |
| DB | 780 | GTGGTCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTC | 824 |

Search completed: May 30, 2006, 03:54:18
Job time : 910.723 secs

TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-940-605A-11

Alignment Scores:
Pred. No.: 5.54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x US-07-940-605A-11 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACAGTGACCGCTTGTCTCGCGTGGCTTGTCTCCAGCGCCGAGG 125
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCAACCCGACGCTGGGCTGCTGCTCTTCAGCGG 245
Qy 61 ArgGlyAlaAlaAsaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGG 305
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGGTGGGGGACACCTTCGTCTC 365
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGACGACTTCCCGCGAGAGACGAGGCTACTATTCTGCTCGGCTTGGAGAAC 425
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 426 TCCATCATGTACTTCAGCCACTTCGTGCGGTTCCTCGCCAGCGAAGCCACACGAGG 485
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGGCGAGCCTGTCTCGTGGC 545
Qy 161 ProGluAlaCysArgProAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGGGGTGCGCGGCCAGCGCGGGCGCGAGTGCACACGAGGGGGCTGACTTCGCC 605
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGCGGCCCTTGGCGGACTTGTGGGGTCTTCTCTGTCACTG 665
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTTACTGCAACACACAGGAACCGAGACGCTGTTTGCATAATGTCCCGGCT 725
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAATCGGGAGACAAGCCCGACCTTTCGGCGAGATACGTC 770

RESULT 2
US-08-690-096-11
; Sequence 11, Application US/08690096
; Patent No. 5945513

GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-690-096-11

Alignment Scores:
Pred. No.: 5.54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x US-08-690-096-11 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACAGTGACCGCTTGTCTCGCGTGGCTTGTCTCCAGCGCCGAGG 125
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCAACCCGACGCTGGGCTGCTGCTGCTTTCAGCGG 245
Qy 61 ArgGlyAlaAlaAsaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGG 305
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGGTGGGGGACACCTTCGTCTC 365
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

Db 366 ACCCTGAGGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCATCATGACTTACGACCACTTCGTGCGGGTCTTCTGCGGAGGAGCCACACGAGC 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCCCGGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTCCCTCGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGCGGTGCGGCCACCGCGGGGGCGGAGTGCACACGAGGGGGCTGGAATTCGCGC 605
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGGCGCCCTTGGCGGGAGCTTGTGGGGTCTTCTCTGTCTG 665
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACAGAACCGAAGACGTGTTTGCAAAATGTCCCGGCT 725
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 3
US-09-023-655-1014
; Sequence 1014, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: g179145
US-09-023-655-1014
Alignment Scores:
Pred. No.: 5,54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-804-763-1 (1-235) x US-09-023-655-1014 (1-1060)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCCCTTACCAGTACGCCCTTGTCTCTGCGCTGCTGCTCCACGCGCCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGTGTGCGCGTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTGCAGGTGCTGCTCCAACCCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCCG 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCGCGCTCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCGAGGGGGTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCGTCTC 365
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGGAGCTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCATCATGACTTTCAGCCACTTCGTGCGGGTCTTCTGCGGAGGAGCCACACGAGC 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTCTCTGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGGGGTGCGGCCACCGCGGGGGCGGAGTGCACACGAGGGGGCTGGAATTCGCGC 605
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGGCGCCCTTGGCGGGAGCTTGTGGGGTCTTCTCTGTCTG 665
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGGCT 725
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 4
US-10-131-831-9109
; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121

; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Alignment Scores:
Pred. No.: 1.01e-104 Length: 2150
Score: 1238.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.3% Indels: 0
DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x US-10-131-831-9109 (1-2150)

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Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCCTTGCTGCTCCACGCCGCCAGG 65

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 66 CCGAGCCAGTTCGGGTGTGCGCGTGGATCGGACCTGGACCTGGGCGAGACAGTGGAG 125

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGGTGCTGCTGTCAACCCGAGCTGGGCTGCTGTGGCTCTTCCAGCG 185

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGCGCGCGCGCGCAGTCCACCTTCCTCTATACCTCTCCCAAAACAGCCCAAGCG 245

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 246 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAGAGAGTGGGGGACACCTTCGTCCTC 305

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 306 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTGCTATTCTGCTCGGCCCTGAGCAAC 365

Qy 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 366 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACACGAGC 425

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 426 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGACCCCTGTCCCTGCGC 485

Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 486 CCAGAGGCGTGC CGGCCCGCGCGGGGCGCAGTGCAACAGAGGGGCTGGACTTCGCC 545

Qy 181 CysAspIleTyrrIleThrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 546 TGTGATATCATCATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTCACTG 605

Qy 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 606 GTTATACCCCTTACTGCAACACAGGAAACCGAGACGTGTTGCAATGTCCTCCCGGCT 665

Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
Db 666 GTGGTCAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 710
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RESULT 5

US-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramer, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified FAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1128
US-08-751-512-7

Alignment Scores:
Pred. No.: 7.41e-79 Length: 1131
Score: 954.00 Matches: 181
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.5% Indels: 0
DB: 3 Gaps: 0

US-10-804-763-1 (1-235) x US-08-751-512-7 (1-1131)

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Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCCTTGCTGCTCCACGCCGCCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGGACCTGGGCGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGTCAACCCGAGCTGGGCTGCTGTGGCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCAGTCCACCTTCCTCTATACCTCTCCCAAAACAGCCCAAGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTTCCTCGGCGAAGAGGTTGGGGGACACCTTCGTCCTC 300
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QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCATCATGTACTTCAGCCACTTCGTGCGCGGTCTTCCTGCCAGCAAGCCACACGACG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACCAACCGCGGCCACCATCGCGTCGAGGCCCTGTCCCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGAGTGCACACGAGGGGGCTGGACTTCGCC 540
QY 181 Cys 181
Db 541 TGT 543

RESULT 6

US-08-403-853-11
; Sequence 11, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide

; LOCATION: 1..819
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 1..819
US-08-403-853-11

Alignment Scores:
Pred. No.: 1.89e-48 Length: 822
Score: 623.00 Matches: 124
Percent Similarity: 94.0% Conservative: 1
Best Local Similarity: 93.2% Mismatches: 2
Query Match: 50.0% Indels: 6
DB: 2 Gaps: 2

US-10-804-763-1 (1-235) x US-08-403-853-11 (1-822)

QY 9 LeuLeuProLeuAla-----LeuLeuLeuHisAlaAlaArgPro-----Ser 22
Db 10 CTATTGCGCTACGCGCAGCGCTGGATTGTTATTACTCGCTGCCCAACCGCATGGCCAGC 69
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 70 CAGTTCGGGTGTCGCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAGCTGAAG 129
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 130 TGCCAGGTGCTGCTGTCCAACCGGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCGCGGC 189
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 190 GCCGCGCGCAGTCCACCTTCCTCTATACCTCTCCCAAAACAAGCCCAAGCGCGCGAG 249
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 250 GGGCTGGACACCCAGCGGTTCTCGGCGAAGAGGTTGGGGGACACCTTCGTCTCCTCCCTG 309
QY 103 SerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db 310 AGCGACTTCCGCGCAGAGAACGAGGGCTACTATTTCGTCTGGCCCTGAGCAACTCCATC 369
QY 123 MetTyrPheSerHisPheValProValPheLeuProAla 135
Db 370 ATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCG 408

RESULT 7

US-09-477-737-2
; Sequence 2, Application US/09477737
; Patent No. 6544506
; GENERAL INFORMATION:
; APPLICANT: Reiser
; TITLE OF INVENTION: VETO CELLS EFFECTIVE IN PREVENTING GRAFT REJECTION AND DEVOID OF
; FILE OF INVENTION: VERSUS HOST POTENTIAL
; FILE REFERENCE: 00/20548
; CURRENT APPLICATION NUMBER: US/09/477,737
; CURRENT FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In ver. 2.1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-477-737-2

Alignment Scores:
Pred. No.: 1.7e-39 Length: 803
Score: 526.00 Matches: 124
Percent Similarity: 62.7% Conservative: 34
Best Local Similarity: 49.2% Mismatches: 72
Query Match: 42.2% Indels: 22
DB: 3 Gaps: 12

US-10-804-763-1 (1-235) x US-09-477-737-2 (1-803)

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Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 13 ATGGCCCTACCGTTGACCGCGTTCTGTCGTGAACCTGCTGCTGGGTGAGTCGATT 72
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 73 ATCTGGGGAGTGAGAGCTAAGCCACAGCACCCGNACTCCGAATCTTCCAAAGAA 132
Qy 31 ArgThrTrpAenLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 133 ATGACGCCGGAACCTTGGTCAGAGCTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 189
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla-----AlaAlaSerProThrPhe 69
Db 190 TCGCAAGGATCTCTTGCTCTTCAGAACTCCAGCTCCAAACTCCCCACGCCACCTTC 249
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 250 GTTGCTATATGGCTTCATCCACACAAAGATAAGTGGGACGAGAGCTGAATCTGTCG 309
Qy 88 Arg----PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 310 AAACCTGTTTTCTGCCATGAGGACACAGCAATAATAAGTAGCTTCTCACCTCAACAAGTTC 369
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 370 AGCAAGGAAACGAAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 429
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 430 AGTTCTGTCGTCGACCTCTTCAGAAAGTGAAGTACTACTACTACCAAGCTGCTGCGA 489
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 490 ACTCCCTCACCTGTGCACCTACCGGGACATCTCAGCCC-----CAGAGACCAAGAT 543
Qy 164 CysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
Db 544 TGTGCGCCCGT-----GGCTCAGTGAAGGGACCGGATTGGACTTCGCTGTGATATT 597
Qy 184 TyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
Db 598 TACATCTGGACACCTTGGCCGGAATCTGCGTGGCCCTTCTGCTGCTTGTATCATCACT 657
Qy 204 LeuTyrCysAenHisArgAsnArgArgValCysLysCysProArgProValValLys 223
Db 658 CTCATCTCTACCAAGGAGCGAAAGCGTGTGCAAAATGTCCAGGCGCGCTAGTCAGA 717
Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 718 CAGGAAGCAAGCCAGACCTTCAGAGAAATTTGTG 753
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RESULT 8

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US-07-940-605A-9
; Sequence 9, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READEABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-940-605A-9

Alignment Scores:
Pred. No.: 2,22e-39 Length: 972
Score: 526.00 Matches: 124
Percent Similarity: 62.7% Conservative: 34
Best Local Similarity: 49.2% Mismatches: 72
Query Match: 42.2% Indels: 22
DB: Gaps: 12

US-10-804-763-1 (1-235) x US-07-940-605A-9 (1-972)
Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 127 ATGGCCCTACCGTTGACCGCGTTCTGTCGTGAACCTGCTGCTGGGTGAGTCGATT 186
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 187 ATCTGGGGAGTGAGAGCTAAGCCACAGCACCCGNACTCCGAATCTTCCAAAGAA 246
Qy 31 ArgThrTrpAenLeuGlyThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 247 ATGACGCCGGAACCTTGGTCAGAGCTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 303
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 304 TCGCAAGGATCTCTTGCTCTTCAGAACTCCAGCTCCAAACTCCCCACGCCACCTTC 363
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 364 GTTGCTATATGGCTTCATCCACAAAGATAAGTGGGACGAGAGCTGAATTCGTCG 423
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 424 AAACCTGTTTTCTGCCATGAGGACACAGCAATAATAAGTAGCTTCTCACCTGAACAAGTTC 483
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 484 AGCAAGGAAACGAAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 544 AGTTCTGTCGTCGACCTTCAGAAAGTGAAGTACTACTACTACCAAGCTGCTGTCGCA 603
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 604 ACTCCCTCACCTGTGCACCTACCGGGACATCTCAGCCC-----CAGAGACCAAGAT 657
Qy 164 CysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
Db 658 TGTGCGCCCGT-----GGCTCAGTGAAGGGACCGGATTGGACTTCGCTGTGATATT 711
Qy 184 TyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeuValIleThr 203
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Db 712 TACATCTGGGACCCCTTGGCGGAATCTGCGTGGCCCTTCTGCTGCTTGTATCATCACT 771
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Qy 204 LeuTyCysAsnHisArgAsnArgArgAtgValCysLysCysProArgProValValLys 223
|||||

Db 772 CTCATCTGTACCACAGGAGCCGAAAGCGGTGGTTCGAAATGTCACAGCCGCTAGTCAGA 831
|||||

Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
|||||

Db 832 CAGGAAGGCAAGCCAGACCTTCAGAGAAATTTGTG 867
|||||

RESULT 9

US-08-690-096-9

; Sequence 9, Application US/08690096

; Patent No. 5945513

; GENERAL INFORMATION:

; APPLICANT: ARUFFO, ALEJANDRO

; APPLICANT: HOLLENBAUGH, DIANE

; APPLICANT: LEDBETTER, JEFFREY A.

; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,096

; FILING DATE: 31-JUL-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/940,605

; FILING DATE: 04-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 5624-184

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090

; TELEFAX: 212 869-9864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 972 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-690-096-9

Alignment Scores:

| Pred. No.: | 2,22e-39 | Length: | 972 |
|------------------------|----------|---------------|-----|
| Score: | 526.00 | Matches: | 124 |
| Percent Similarity: | 62.7% | Conservative: | 34 |
| Best Local Similarity: | 49.2% | Mismatches: | 72 |
| Query Match: | 42.2% | Indels: | 22 |
| DB: | 2 | Gaps: | 12 |

US-10-804-763-1 (1-235) x US-08-690-096-9 (1-972)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
|||||

Db 127 ATGGGCTCACCGTTGACCGCTTCTGCTGCTGAACCTGCTGCTGCTGGGTGAGTCGATT 186
|||||

Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
|||||

Alignment Scores:

Db 187 ATCTGGGGAGTGGAGAACTAAGCCACAGGACCCGAACTCCGAATCTTTCCAAAGAAA 246
|||||

Qy 31 ArgThrTrrAsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
|||||

Db 247 ATGGACGCCGAACCTTGGTCAGAAAGGTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 303
|||||

Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
|||||

Db 304 TCGCAAGGATGCTCTTGGCTCTTCCAGAACTCCAGCTCCAAACTCCCCAGGCCACCTTC 363
|||||

Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
|||||

Db 364 GTTGTCTATATGCTTTCATCCCAACAAGATAAAGTGGGACGAGAGAGCTGAATTCGTCG 423
|||||

Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
|||||

Db 424 AAACGTGTTTCTGCCATGAGGACACAGATAATAAGTACGTTCTCACCTTGAACAAGTTC 483
|||||

Qy 106 ArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
|||||

Db 484 AGCAAGGAAACGAAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543
|||||

Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
|||||

Db 544 AGTTCTGTCGCCAGTCTCTTCAGAAAGTCAACTCTACTACTACCAAGCCAGCTGCTGCGA 603
|||||

Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
|||||

Db 604 ACTCCTCTACCTGTGCGACCCCTACCGGACATCTCAGCCC-----CAGAGACCAGAGAT 657
|||||

Qy 164 CysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
|||||

Db 658 TGTGGGCCCGT-----GGCTCAGTGAAGGGGACCGGATTTGACTTCGCTGTGATATT 711
|||||

Qy 184 TyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
|||||

Db 712 TACATCTGGGACCCCTTGGCCGGAATCTGCTGGCCCTTCTGCTGTCTTGATCATCACT 771
|||||

Qy 204 LeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgProValValLys 223
|||||

Db 772 CTCATCTGTACACAGGAGCCGAAAGCGTGTTCGAATGTCCAGGCCGCTAGTCAGA 831
|||||

Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
|||||

Db 832 CAGGAAGGCAAGCCAGACCTTCAGAGAAATTTGTG 867
|||||

RESULT 10

US-09-966-976A-8/c

; Sequence 8, Application US/09966976A

; Patent No. 6953688

; GENERAL INFORMATION:

; APPLICANT: Ferrick, David A.

; APPLICANT: Swift, Susan E.

; APPLICANT: Armstrong, Randall

; APPLICANT: Fox, Bryan

; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and Ige Sy

; FILE OF INVENTION: Secretion and Switch Rearrangement

; CURRENT APPLICATION NUMBER: US/09/966,976A

; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US 09/076,624

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 8345

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic

US-09-966-976A-8

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-076-624-8

Alignment Scores:
Pred. No.: 1.15e-18 Length: 8345
Score: 316.00 Matches: 94
Percent Similarity: 53.3% Conservatives: 42
Best Local Similarity: 36.9% Mismatches: 81
Query Match: 25.3% Indels: 38
DB: Gaps: 15

US-10-804-763-1 (1-235) x US-09-966-976A-8 (1-8345)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14
Db 4974 ATGCGCTCACCGTTGACCGCGCTTCTGCTGCTGAACCTGCTGCTGGGTGAGTCGATT 4915
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 4914 ATCTGGGGAGTGAGAGCTAAGCAGCAGCAGCCGCACTCCGAATCTTTCCAAAGAAA 4855
Qy 31 ArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 4854 ATGACGCGCAACTTGGTCAGAAGGTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 4798
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 4797 TCGCAAGGATGCTCTTGCTCTCCAGAACTCCAGCTCCAACTCCCGCCAGCCCTTC 4738
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 4737 GTTGTCTATATGGCTTCATCCCAACAAGATAAGTGGGAGAGAGCTGAATTCGTCG 4678
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 4677 AAACGTGTTTCTGCCATGAGGACAGCAATAAAGTACGTTCTCACCTGAACAAGTTC 4618
Qy 106 ArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 4617 AGCAAGGAAAACGAAGGCTACTATTCTGCTCAGTCATCAGCAACTCCCGACCTGATGACTTC 4558
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 4557 AGTTCTGTCGTCAGTCTCTCAGAAAGTGAACCTACTACTACTACCAAGCCAGTGTGCGA 4498
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 4497 ACTCCCTCACCTGTGACCCCTACCGGGACATCTCAGCCC-----CAGAGACCAGAAGAT 4444
Qy 164 CysArgProAlaAlaGlyAlaValHisThrArgGly-----LeuAspPheAlaCys 181
Db 4443 TGTGCGCCCGCT-----GGCTCAGTGAAGGGGACCGGAAACCGGTTGGGTGGCTTTGT 4390
Qy 182 AspileTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuVal 201
Db 4389 -----CTTCTCTTTTGCCTTCCCAATCCA 4369
Qy 202 IleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgProVal 221
Db 4368 CTAATTGTTGGTGAAGAAAGAAAGTACAGAAAACATGCAAGAAAGCAGACAGAAAGAA 4309
Qy 222 ValLys---SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 4308 AACCAAGGTCTCATGAATCTCCAACTTAATCTCTGAACAGTGT 4264

RESULT 12
US-08-403-853-9
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; Sequence 9, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORBT, Alex A.
; APPLICANT: KORBT, Robert A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..840
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..840
; US-08-403-853-9

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Pred. No.: 1,148-13 Length: 849
Score: 247.00 Matches: 62
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Query Match: 19.8% Indels: 16
DB: Gaps: 7

US-10-804-763-1 (1-235) x US-08-403-853-9 (1-849)
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QY 23 -----GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThr 38
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; Sequence 9, Application US/09596774
; Patent No. 6984382
; GENERAL INFORMATION:
; APPLICANT: GRONER, BERND
; APPLICANT: MORITZ, DIRK
; TITLE OF INVENTION: BIFUNCTIONAL PROTEIN, PREPARATION AND USE
; FILE REFERENCE: 24741-1521
; CURRENT APPLICATION NUMBER: US/09/596,774
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/159,027
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 08/793,048
; PRIOR FILING DATE: 1996-11-01
; PRIOR APPLICATION NUMBER: PCT/EP95/01494
; PRIOR FILING DATE: 1995-04-20
; PRIOR APPLICATION NUMBER: EP 94810244.7
; PRIOR FILING DATE: 1994-05-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 5
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: chimeric nucleotide sequence
; NAME/KEY: CDS
; LOCATION: (40)..(1422)
; US-09-596-774-5

Alignment Scores:
Pred. No.: 1,038-08 Length: 1479
Score: 197.00 Matches: 76
Percent Similarity: 43.9% Conservative: 35
Best Local Similarity: 30.0% Mismatches: 99
Query Match: 15.8% Indels: 45
DB: Gaps: 12

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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 509 CCCAGTCTCACAAATTCCTGTCTCCACTTCA-----GTAGAGACAGGGGTCAAGC 555
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Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
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   ::::::::::::::::::::
Qy 61 ArgGlyAlaAlaLeuSerProThrPheLeuLeuValLeuSerGlnAsnLysProLysAla 80
   ::::::::::::::::::::
Db 613 CCAGA-----CAATCTCTAACTTCTGATTACTCGGCATCTCCCGGTACTACTGA 666
   ::::::::::::::::::::
Qy 81 AlaGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
   ::::::::::::::::::::
Db 667 GTC-----CCTTCTCGTTCACTGGCAGTGGCTCTGGGCCGGATTTCATTTC 714
   ::::::::::::::::::::
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSer----- 116
   ::::::::::::::::::::
Db 715 ACCATCAGCAGTGTGCGAGCTGAAGACCTGCGAGTTTATTCTGTGCAACATTTTGT 774
   ::::::::::::::::::::
Qy 117 ----- 120
   ::::::::::::::::::::
Db 775 ACTCCATTCACTTCGGCTCGGGACAAAATTGGAGATCAAGCTCTAGAGATCAGCAAC 834
   ::::::::::::::::::::
Qy 121 SerLeuMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
   ::::::::::::::::::::
Db 835 TCGGTGATGTTACTTTCAGTTCTGTGCGCAGTCTCTCAGAAAGTGAACCTCTACTACT 894
   ::::::::::::::::::::
Qy 141 ---ProAlaProArgProProThrProAla---ProThrIleAlaSerGlnProLeuSer 158
   ::::::::::::::::::::
Db 895 AAGCAGGTGTCGGAACCTCCCTCAGTGTGACCCCTACCGGACATCTCAGCCC----- 948
   ::::::::::::::::::::
Qy 159 LeuArgProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAsp 178
   ::::::::::::::::::::
Db 949 CAGAGACAGAGATTGTGCGCCCGT-----GGCTCAGTGAAGGGACCGGATTGGAC 1002
   ::::::::::::::::::::
Qy 179 PheAlaCysAspIleTyrrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeu 198
   ::::::::::::::::::::
Db 1003 TTTCTAGAGGATCCCAAACTCTGCTACTTGTCTAGATGGAATC-----CTCTTCATCTAC 1056
   ::::::::::::::::::::
Qy 199 SerLeuValIleThr---LeuTyrrCysAsnHisArgAsnArgArgArgValCysLysCys 217
   ::::::::::::::::::::
Db 1057 GGAGTGCATCATCAGACCCCTGTACTGTAGAGCAAAATTCAGCAGGATGTCAGA-GACTGC 1115
   ::::::::::::::::::::
Qy 218 ProArgProValValLysSerGlyAspLysProSerLeu 230
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Db 1116 TGCCAACT-----GCAGGACCCCAACACGCTCTA 1145
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RESULT 14

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US-08-751-359-21
; Sequence 21, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
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; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-751-359-21

Alignment Scores:      0.035      Length:      5526
Pred. NO.:            135.00      Matches:      78
Score:                39.6%      Conservative: 32
Percent Similarity:   28.1%      Mismatches:  80
Best Local Similarity: 10.8%      Indels:      91
Query Match:          3          Gaps:         18
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US-10-804-763-1 (1-235) x US-08-751-359-21 (1-5526)

Qy 7 AlaLeuLeuLeuProLeuAla-----LeuLeuLeuHisAlaAla----- 19
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Qy 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
   ::::::::::::::::::::
Db 664 CAGCGGTCTCGGTGTGAGCAAAACCG-----GGAGAAACCGTCT 702
   ::::::::::::::::::::
Qy 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
   ::::::::::::::::::::
Db 703 AAGATCATCCTGTC-----TCCGGGATAGGAGCTACTATGGCTGG---TACCAG 747
   ::::::::::::::::::::
Qy 60 ProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLys 79
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Db 748 CAGAGGACCTGCGAGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 807
   ::::::::::::::::::::
Qy 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
   ::::::::::::::::::::
Db 808 GACATC-----CCTTCAGATTCTCCGGTTCCAAATCCGGCTCCACAGCCACA 855
   ::::::::::::::::::::
Qy 100 LeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrrPheCysSerAlaLeu--- 118
   ::::::::::::::::::::
Db 856 TTAACCATCACTGGGTGTCAGACCGCAGCAGGCTGTCTATTACTGTGGAGTGC-AGA 914
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Qy 119 -----SerAsn----- 120
   ::::::::::::::::::::
Db 915 CAGCAGCATGTTCTGTCGACCGTGCACAAAGCAATGGGAAATGATACAAAACCTCCT 974
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Qy 121 -----SerIleMetTyrrPheSerHisPhe--- 128
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Qy 129 ---ValProValPheLeu-----ProAlaLysProThrThrThrProAlaPro 143
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Db 1035 TCCTGCCCTGTGTGTCGACGCGCCGGTCTCTCTCGTTTCCCGAGGTGCACCCAGGTCCA 1094
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Qy 169 GlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIleTyrrIle---TrpAla 187
   ::::::::::::::::::::
Db 1212 GAGGGCCACCACTCAATTGCACTG-----TACATCAGCAGCAGCA 1253
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Qy 188 ProLeuAlaGlyThrCysGlyValLeu-----LeuLeuSerLeuValIleThrLeuTyrr 205
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Db 1254 CCAGTTCTCTT-ACATGTGTCCCTGTGAGAAAGAGCTGGACTTCTTAAGCACCCCTTAG- 1311
QY 206 CysAsnHisArg-----AsnArgArgValCysLysCysProArg 219
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US-08-907-146-21

; Sequence 21, Application US/08907146

; Patent No. 6316600

; GENERAL INFORMATION:

; APPLICANT: Michael, Nancy M

; APPLICANT: Accavitti, Marianne

; APPLICANT: Thompson, Craig B

; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/907,146

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/751,359

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: ARSB:504

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512/418-3000

; TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5526 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-907-146-21

Alignment Scores:

| | | | |
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| Pred. No.: | 0.035 | Length: | 5526 |
| Score: | 135.00 | Matches: | 78 |
| Percent Similarity: | 39.6% | Conservative: | 32 |
| Best local Similarity: | 28.1% | Mismatches: | 80 |
| Query Match: | 10.8% | Indels: | 91 |
| DB: | 3 | Gaps: | 18 |

US-10-804-763-1 (1-235) x US-08-907-146-21 (1-5526)

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QY 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
Db 664 CAGCGGTCTCGGTGTGAGAAACCG-----GGAGAAACCGTC 702
QY 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
Db 703 AAGATCACCTGC-----TCCGGGGATAGAGGCTACTATGGCTGG---TACCAG 747

QY 60 ProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrLeuSerGlnAsnLysProLys 79
Db 748 CAGAAGGCACCTGGCAGTGCCTCTGTCTACTGTGATCTATGCTAACCAACACACCCCTCG 807
QY 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
Db 808 GACATC-----CCTTCACGATTCTCCGGTTCACAAATCCCGCTCCACAGCCACA 855
QY 100 LeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTrPheCysSerAlaLeu--- 118
Db 856 TTAACCATCACTGGGGTCCAAGCCGACGACGAGGCTGTCTATTACTGTGGAGTGC-AGA 914
QY 119 -----SerAsn----- 120
Db 915 CAGCAGCAGTACTGTCTGCACGGTGACACAAAGCAATGGGGAATGATACAAAAACCTCT 974
QY 121 -----SerIleMetTyTrPheSerHisPhe--- 128
Db 975 GCCAGTGAAGGAGCAGCTGATGGTTTACTGTCTCTGTCTTACAAAGTCCCACTCCCAT 1034
QY 129 ---ValProValPheLeu-----ProAlaLysProThrThrThrProAlaPro 143
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QY 144 -----ArgProPro-----ThrProAlaProThrIle 152
Db 1095 GCTGGCTGAATCCCTGCCATCAACATCCACCATTTGTAGTGTCCCTGCATGCACCA 1154
QY 153 AlaSerGlnPro-----LeuSerLeuArgProGluAlaCysArgProAlaAla 168
Db 1155 CTGGCAGCTCCTCATCTGCTCTCCCTCCCACTGAGACCACCTGCC---CAGCCCATGCTG 1211
QY 169 GlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIleTyTrIle---TrpAla 187
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QY 188 ProLeuAlaGlyThrCysGlyValLeu-----LeuLeuSerLeuValIleThrLeuTy 205
Db 1254 CCAGTTCTCTT-ACATGTGTCTCTGAGGAAAGAGCTGGACTTCTTAAGCACCCCTTAG- 1311
QY 206 CysAsnHisArg-----AsnArgArgValCysLysCysProArg 219
Db 1312 TGTACTCACCTAAATGAAACTGAAACCCCATAAAGTCTCAGAAATACCCAGA 1365

Search completed: May 29, 2006, 12:46:40

Job time : 263.367 secs

GenCore version 5.1.8
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Run on: May 30, 2006, 04:14:31 ; Search time 1318.82 Seconds
(without alignments)

3284.288 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA_Main:

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
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- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| | | | | | |
|----|--------|-------|------|----|--------------------|
| 2 | 1247 | 100.0 | 708 | 10 | US-10-804-763-28 |
| 3 | 1247 | 100.0 | 1060 | 6 | US-10-207-655-173 |
| 4 | 1247 | 100.0 | 1060 | 8 | US-10-641-643-1014 |
| 5 | 1247 | 100.0 | 2261 | 9 | US-10-804-762-2 |
| 6 | 1247 | 100.0 | 2261 | 10 | US-10-888-313A-99 |
| 7 | 1247 | 100.0 | 2261 | 10 | US-10-804-763-2 |
| 8 | 1167 | 93.6 | 692 | 7 | US-10-378-393-2 |
| 9 | 1167 | 93.6 | 1995 | 7 | US-10-378-393-6 |
| 10 | 1166.5 | 93.5 | 2411 | 7 | US-10-378-393-10 |
| 11 | 1162 | 93.2 | 689 | 7 | US-10-378-393-19 |
| 12 | 1162 | 93.2 | 690 | 7 | US-10-378-393-12 |
| 13 | 1162 | 93.2 | 1987 | 7 | US-10-378-393-17 |
| 14 | 1162 | 93.2 | 8858 | 7 | US-10-378-393-1 |
| 15 | 1149.5 | 92.2 | 2134 | 9 | US-10-723-860-5746 |
| 16 | 1094 | 87.7 | 708 | 9 | US-10-804-762-26 |
| 17 | 1094 | 87.7 | 708 | 10 | US-10-804-763-26 |
| 18 | 1008.5 | 80.9 | 597 | 9 | US-10-804-762-6 |
| 19 | 1008.5 | 80.9 | 597 | 10 | US-10-804-763-6 |
| 20 | 1006.5 | 80.7 | 2150 | 9 | US-10-804-762-4 |
| 21 | 1006.5 | 80.7 | 2150 | 10 | US-10-804-763-4 |
| 22 | 809 | 64.9 | 785 | 9 | US-10-804-762-22 |
| 23 | 809 | 64.9 | 785 | 10 | US-10-804-763-22 |
| 24 | 708.5 | 56.8 | 2001 | 9 | US-10-804-762-18 |
| 25 | 708.5 | 56.8 | 2001 | 10 | US-10-804-763-18 |
| 26 | 695.5 | 55.8 | 2179 | 9 | US-10-804-762-20 |
| 27 | 695.5 | 55.8 | 2179 | 10 | US-10-804-763-20 |
| 28 | 655 | 52.5 | 1330 | 9 | US-10-804-763-16 |
| 29 | 655 | 52.5 | 1330 | 10 | US-10-804-763-16 |
| 30 | 601 | 48.2 | 1229 | 9 | US-10-804-762-24 |
| 31 | 601 | 48.2 | 1229 | 10 | US-10-804-763-24 |
| 32 | 562.5 | 45.1 | 1010 | 9 | US-10-804-763-14 |
| 33 | 562.5 | 45.1 | 1010 | 10 | US-10-804-762-14 |
| 34 | 562.5 | 45.1 | 1010 | 16 | US-11-136-537-2941 |
| 35 | 526 | 42.2 | 803 | 3 | US-09-477-737-2 |
| 36 | 523 | 41.9 | 1452 | 9 | US-10-804-762-10 |
| 37 | 523 | 41.9 | 1452 | 10 | US-10-804-763-10 |
| 38 | 517 | 41.5 | 744 | 9 | US-10-804-762-12 |
| 39 | 517 | 41.5 | 744 | 10 | US-10-804-763-12 |
| 40 | 494 | 39.6 | 933 | 9 | US-10-804-762-8 |
| 41 | 494 | 39.6 | 933 | 9 | US-10-804-762-30 |
| 42 | 494 | 39.6 | 933 | 10 | US-10-804-763-8 |
| 43 | 494 | 39.6 | 933 | 10 | US-10-804-763-30 |
| 44 | 471.5 | 37.8 | 922 | 7 | US-10-311-455-2246 |
| 45 | 471.5 | 37.8 | 922 | 7 | US-10-240-485-186 |

ALIGNMENTS

RESULT 1
US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransjection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804/762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Alignment Scores: 3.17e-125 Length: 708
Pred. No.: 1247.00 Matches: 235

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Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-762-28 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCCTTACCAGTGACCGGCTTCTCTCGCGCTGGGCTTGTCTCCACGCCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCGCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCCAGCGAAGCCCAAGGCG 420
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTCGCACACGAGGGGCTGGACTTCGCC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGCGTCCGCGCCAGCGCGGGGGCGGACGAGTGCACACGAGGGGGCTGGACTTCGCC 540
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACGTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCCCTTACTGCAACACAGGAACCGAAGACGTGTTTGCANAATGTCCCCGGCCT 660
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 705

RESULT 2
US-10-804-763-28
; Sequence 28, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; PRIORITY FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-28
Alignment Scores: 3.17e-125 Length: 708
Pred. No.: 1247.00 Matches: 235
Score: 1247.00 Mismatches: 0
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-763-28 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCCTTACCAGTGACCGGCTTGTCTCTCGCGCTGGGCTTGTCTCCACGCCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCGCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCCAGCGAAGCCCAAGGCG 420
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTCGCACACGAGGGGCTGGACTTCGCC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGCGTCCGCGCCAGCGCGGGGGCGGACGAGTGCACACGAGGGGGCTGGACTTCGCC 540
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACGTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCCCTTACTGCAACACAGGAACCGAAGACGTGTTTGCANAATGTCCCCGGCCT 660
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 705

RESULT 3
US-10-207-655-173
; Sequence 173, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
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NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 173
LENGTH: 1060
TYPE: DNA
ORGANISM: Homo sapiens
US-10-207-655-173

Alignment Scores:
Pred. No.: 5,33e-125 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-1 (1-235) x US-10-207-655-173 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 66 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyValGlu 40
DB 126 CCGAGCCAGTTCGGGTGTCGGCTGGATCGACCTGGAACTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTCCAGTGTCTGTCCAAACCGAGCTGGGCTGTCTGGCTCTTCCAGCGG 245
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
DB 246 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGCTGGACACCGAGGGTCTCGGCAAGAGGTGGGGGACACCTTCGCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
DB 366 ACCGTAGCGGACTTCGGCGGAGAGAACGAGGGCTACTATTCTCGGCCCTTGAGCAAC 425
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 426 TCCATCATGTACTTCAGGCACCTTCGTGGCGGTCTTCTGCCAGCGAAAGCCACGACG 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCGAGCGCGCGACCAACACCGCGGCCACCATCGCGTGGCGGCTGTCTCTCTGTCACTG 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 546 CCAGAGGGCTGCCGCGCAGCGCGGGGGGCGAGTGCACACAGGGGGCTGAGCTTCGCC 605
QY 181 CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
DB 606 TGTGATATCTACATCTGGCGGCGCTTGGCGGAGCTTGGGGGTCTCTCTCTGTCACTG 665
QY 201 ValIleThrLeuTyCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
DB 666 GTTATCACCTTTTACTGCAACACACAGGAACCGAAGACGTGTTTGAATATGTCCTCCG 725
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
DB 726 GTGTCAATTCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 4

US-10-641-643-1014
Sequence 1014, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart

Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1014:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: g179145
LIBRARY: GENBANK
SEQUENCE DESCRIPTION: SEQ ID NO: 1014 :
US-10-641-643-1014

Alignment Scores:
Pred. No.: 5,33e-125 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-804-763-1 (1-235) x US-10-641-643-1014 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 66 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyValGlu 40
DB 126 CCGAGCCAGTTCGGGTGTCGGCTGGATCGACCTGGAACTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTCCAGTGTCTGTCCAAACCGAGCTGGGCTGTCTGGCTCTTCCAGCGG 245
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
DB 246 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGCTGGACACCGAGGGTCTCGGCAAGAGGTGGGGGACACCTTCGCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120

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Db 366 ACCGTGACGACTTCCGCGGAGAACAGAGGCTTACTATTCTGCTGGCCCTGAGCAAC 425
Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTACGCCACTTTCGTCCGGTCTTCTGCCAGCGAAGCCACACGACG 485
Qy 141 ProAlaProArgProProThrProAlaProThrThrLeuAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGGACACCAACACCGCGGCCACCACTCGCTCGCAGCCCTGTCCCTGCGC 545
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGCGTCCCGCGCAGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTCGCC 605
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTCACTG 665
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCMAATGTCCCGGCT 725
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 770

RESULT 5
US-10-804-762-2
; Sequence 2, Application US/10804762
; Publication No. US2005004221A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransjection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-2

Alignment Scores:
Pred. No.: 1.41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-762-2 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCGCTTACCAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCTCCAGCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTGCGCGGTGGATCGAACCCTGGACCTGGCGGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGTGTCACACCGACGTCGCGGTGCTGTCTTCCAGCGC 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 120 ATGGCGCTTACCAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCTCCAGCGCAGG 179
```

```
Db 300 CGCGCGCGCGCGCGAGTCCACCTTCTCTCTATACCTTCTCCCAAAACAAGCCCAAGCGC 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCGTGACGACTTCCCGCGGAGAACAGAGGCTTACTATTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTACGCCACTTTCGTCCGGTCTTCTGCCAGCGAAGCCACACGACG 539
Qy 141 ProAlaProArgProProThrProAlaProThrThrLeuAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGGACACCAACACCGCGGCCACCACTCGCTCGCAGCCCTGTCCCTGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGTCCCGCGCAGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTCGCC 659
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTCACTG 719
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCMAATGTCCCGGCT 779
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 824

RESULT 6
US-10-888-313A-99
; Sequence 99, Application US/10888313A
; Publication No. US20050100934A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Kevin
; APPLICANT: AXEL, Richard
; APPLICANT: STRAPPS, Walter
; APPLICANT: BARNEA, Gilad
; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction
; FILE REFERENCE: SENTI 203.2
; CURRENT APPLICATION NUMBER: US/10/888,313A
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/566,113
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60/511,918
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,968
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 99
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-888-313A-99

Alignment Scores:
Pred. No.: 1.41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x US-10-888-313A-99 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCGCTTACCAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCTCCAGCGCAGG 179
```

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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGGCGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTGTCCTCAACCCGAGCTCGGGTGTCTGTGGCTCTTCCAGCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 300 CGCGGGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTGGGGGACACCTTGTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTGGCCCTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCCGTCTTCTGCCAGGAGCCCAAGGCG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGAGCCACCAACACCGCGCCACCATCGCGTGCAGGCCCTGTCTCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 600 CCAGAGGGCGTGGCGGCGAGCGGGGGCGAGTGCACACAGAGGGGCTGGACTTCGCC 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
DB 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTGCAC 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
DB 720 GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGTGTTCGAAATGTCCCGGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
DB 780 GTGGTCAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 824
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RESULT 7

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US-10-804-763-2
; Sequence 2, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-804-763-2

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Alignment Scores:
Pred. No.: 1,41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-763-2 (1-2261)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 120 ATGGGCTTACCAAGTACCGCTTGTCTCTCGCGCTGGCTTGTCTCCACGCGCAG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTGTCCTCAACCCGAGCTCGGGTGTCTGTGGCTCTTCCAGCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 300 CGCGGGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTGGGGGACACCTTGTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTGGCCCTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCCGTCTTCTGCCAGGAGCCCAAGGCG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGAGCCACCAACACCGCGCCACCATCGCGTGCAGGCCCTGTCTCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 600 CCAGAGGGCGTGGCGGCGAGCGGGGGCGAGTGCACACAGAGGGGCTGGACTTCGCC 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
DB 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTGCAC 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
DB 720 GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGTGTTCGAAATGTCCCGGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
DB 780 GTGGTCAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 824
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RESULT 8

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US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 692
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-2

Alignment Scores:
  Pred. No.:      1,53e-116      Length:      692
  Score:          1167.00        Matches:      219
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%    Mismatches: 0
  Query Match:      93.6%        Indels:      0
  DB:               7           Gaps:        0

US-10-804-763-1 (1-235) x US-10-378-393-2 (1-692)

Qy  1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
Db  36 ATGGCCTTACCAGTGACCGCTTGTCTCGCGCTGGCTTGTCTGTCTCCAGCGCCAGG 95

Qy  21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db  96 CCGAGCCAGTTCCCGGGTGTCCCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 155

Qy  41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db  156 CTGAAGTCCAGGTGCTGTCTCCAAACCGACGTGGGCTGCTCGTGGCTCTTCCAGCGG 215

Qy  61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAla 80
Db  216 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 275

Qy  81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db  276 GCCGAGCGGCTGGACACCGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCTC 335

Qy  101 ThrLeuSerAspPheArgGluAsnGluGlyTyrlTyrlPheCysSerAlaLeuSerAsn 120
Db  336 ACCCTGACGCTTCCGCGGAGACGAGGGCTACTATTCTGTCTGGGCGCTGAGCAAC 395

Qy  121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db  396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTCCGAGCAAGCCCAACGACG 455

Qy  141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db  456 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTCGCAGCCCTGTCTCTGCTGCGC 515

Qy  161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db  516 CCAGAGGCGTCCGCGCACGCGGGGGCGGCGAGTGACACAGAGGGGCTGGACTTCGCC 575

Qy  181 CysAspIleTyrlIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db  576 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 635

Qy  201 ValIleThrLeuTyrlCysAsnHisArgAsnArgArgValCysLysCysProArg 219
Db  636 GTTATCACCCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAAATGCCCCGG 692

RESULT 9
US-10-378-393-6
; Sequence 6, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
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; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-6

Alignment Scores:
  Pred. No.:      5,95e-116      Length:      1995
  Score:          1167.00        Matches:      219
  Percent Similarity: 100.0%      Conservative: 0
  Best Local Similarity: 100.0%    Mismatches: 0
  Query Match:      93.6%        Indels:      0
  DB:               7           Gaps:        0

US-10-804-763-1 (1-235) x US-10-378-393-6 (1-1995)

Qy  1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
Db  53 ATGGCCTTACCAGTGACCGCTTGTCTCGCGCTGGCTTGTCTGTCTCCAGCGCCAGG 112

Qy  21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db  113 CCGAGCCAGTTCCCGGGTGTCCCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 172

Qy  41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db  173 CTGAAGTCCAGGTGCTGTCTCCAAACCGACGTGGGCTGCTCGTGGCTCTTCCAGCGG 232

Qy  61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAla 80
Db  233 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 292

Qy  81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db  293 GCCGAGCGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCTC 352

Qy  101 ThrLeuSerAspPheArgGluAsnGluGlyTyrlTyrlPheCysSerAlaLeuSerAsn 120
Db  353 ACCCTGAGCGACTTCGCGCGAGACGAGGGCTACTATTCTGTCTGGGCTTCCAGCAAC 412

Qy  121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db  413 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTCCGAGCAAGCCCAACGACG 472

Qy  141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db  473 CCAGCGCGCGACCAACACCGCGCGCCACCATCGGTGCGAGCCCTGTCTCTGCTGCGC 532

Qy  161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db  533 CCAGAGGCGTCCGCGCACGCGGGGGCGGCGAGTGACACAGAGGGGCTGGACTTCGCC 592

Qy  181 CysAspIleTyrlIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db  593 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 652

Qy  201 ValIleThrLeuTyrlCysAsnHisArgAsnArgArgValCysLysCysProArg 219
Db  653 GTTATCACCCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAAATGCCCCCG 709

RESULT 10
US-10-378-393-10
; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
```



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; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.:      8 6e-116      Length:      2411
Score:          1166.50      Matches:      222
Percent Similarity: 91.8%      Conservative: 2
Best Local Similarity: 91.0%      Mismatches: 5
Query Match:    93.5%      Indels:      15
DB:             7          Gaps:      1

US-10-804-763-1 (1-235) x US-10-378-393-10 (1-2411)

QY      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      36  ATGGCCTTACCAGTACCGCCTTGCTCTCGCGCTGGCCTTCTGCTCCACCGCCGAGG 95
QY      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      96  CCGAGCCAGTTCCGGGTGTGCGCGTGGATCGAGCTGGAACTGGCGGAGACAGTGGAG 155
QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      156  CTGAAGTGCAGGTGCTGCTGTCACCGAGCTGGGCTGCTCGGGCTCTTCCAGCGG 215
QY      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      216  CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTTCTCCAAAACAGGCCCAAGGCG 275
QY      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      276  GCCAGGGGCTGTGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCTCTC 335
QY      101  ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db      336  ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAAC 395
QY      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      396  TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGGAGGCCACACAGAGG 455
QY      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      456  CCAGCGCGCGAGACCAACACCGCGCCACCATCGGTGCGACACGAGGGGCTGAGCTCG 515
QY      161  ProGluAlaCysArgProAlaAlaGlyThrCysGlyValLeuLeuLeuSerLeu 180
Db      516  CCAGAGGGCTGCGCGCCAGCGCGGGGCGAGTGCACACGAGGGGCTGAGCTTCGCG 575
QY      181  CysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db      576  TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCTG 635
QY      201  ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro----- 218
Db      636  GTTATCACCTTTTACTGTCAACACAGAACCGAGCGGTGTTGCAATGTCCTCCCTCGAG 695
QY      219  -----ArgProValValLysSerGly 225
Db      696  TCTACGATGCGGAGACTGCTCGAGAAACGGAGCTGGTGGAGCCGCTGACACCTAGCGGA 755

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QY      226  AspLysProSer 229
Db      756  GCGATGCCCAAC 767

RESULT 11
US-10-378-393-19
; Sequence 19, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-19

Alignment Scores:
Pred. No.:      5 3e-116      Length:      689
Score:          1162.00      Matches:      218
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    93.2%      Indels:      0
DB:             7          Gaps:      0

US-10-804-763-1 (1-235) x US-10-378-393-19 (1-689)

QY      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      36  ATGGCCTTACCAGTACCGCCTTGCTCTCGCGCTGGCCTTCTGCTCCACCGCCGAGG 95
QY      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      96  CCGAGCCAGTTCCGGGTGTGCGCGTGGATCGAGCTGGAACTGGCGGAGACAGTGGAG 155
QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      156  CTGAAGTGCAGGTGCTGCTGTCACCGAGCTGGGCTGCTCGGGCTCTTCCAGCGG 215
QY      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      216  CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTTCTCCAAAACAGGCCCAAGGCG 275
QY      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      276  GCCAGGGGCTGTGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCTGTC 335
QY      101  ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db      336  ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAAC 395
QY      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      396  TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGGAGGCCACACAGAGG 455
QY      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      456  CCAGCGCGCGAGACCAACACCGCGCCACCATCGGTGCGACACGAGGGGCTGAGCTCG 515
QY      161  ProGluAlaCysArgProAlaAlaGlyThrArgGlyAlaValHisThrArgGlyLeuAspPheAla 180

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Db 516 CCAGAGCGTCCCGCCAGCGCGGGGGCCAGTGCACAGGGGGCTGGACTTCGCC 575
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 576 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTTGTGGGGTCCCTTCTCTGTCACTG 635
Qy 201 VallleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 636 GTTATCACCCCTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAATGTCCC 689

RESULT 12
US-10-378-393-12
; Sequence 12, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-12

Alignment Scores:
Pred. No.: 5,31e-116 Length: 690
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-12 (1-690)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 36 ATGGCTTTACAGTACCGCCCTTGTCTCTCGCTGGCTTGTGCTCCAGCGCCAGG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCGGGTGTCCGGCTGGATCGGACCTCGAACCTGGGCGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 215
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGC 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGGCTGGACACCGCGGTCTCTCGGCAAGAGGTTGGGGGACACCTTCGTCTCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGACGCTTCCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 395
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCTGTCGGGTCTTCTTCCGAGCGAAGCCCAACACGAGC 455
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Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACACCAACACACCGGCCCCACCATCGCGTCGACAGCCCTGTCCCTGGGC 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 516 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGACGTGCACACGAGGGGCTGGACTTCGCC 575
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 576 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTTGTGGGGTCCCTTCTCTGTCACTG 635
Qy 201 VallleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 636 GTTATCACCCCTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAATGTCCC 689

RESULT 13
US-10-378-393-17
; Sequence 17, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-17

Alignment Scores:
Pred. No.: 2,07e-115 Length: 1987
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-17 (1-1987)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 37 ATGGCTTTACAGTACCGCCCTTGTCTCTCGCTGGCTTGTGCTCCAGCGCCAGG 96
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 97 CCGAGCCAGTTCCGGGTGTCCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 156
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 157 CTGAAGTCCAGGTGCTGCTGTCCAAACCGGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 216
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 217 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGC 276
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 277 GCCGAGGGGGCTGGACACCGCGGTCTCTCGGCAAGAGGTTGGGGGACACCTTCGTCTCTC 336
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
```

```
Db 337 ACCCTGAGGACTTCGCGCAGAGAAACGAGGGCTACTATTTCCTCGGCCCTGAGCAAC 396
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 397 TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCCTGCCAGCGAAGCCACGACG 456
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 457 CCAGCGCCGCGACCAACACCGCGGCCACCATCGCTCGCAGCCCTGTCTCCCTGCGC 516
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuaspPheAla 180
Db 517 CCAGAGCGGTGCGCGCCAGCGCGGGCGCGAGTGCACACGAGGGGGTGGACTTCGCC 576
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 577 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCTG 636
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 637 GTTATCACCCCTTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCC 690

RESULT 14
US-10-378-393-1
; Sequence 1, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-1

Alignment Scores:
Pred. No.: 1.41e-114 Length: 8858
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-1 (1-8858)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6321 ATGGCCCTTACCAGTGACCGCCCTTGCTCGCGCTGGCCCTTCTGCTCCACGCCGCCAGG 6380
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 6381 CCGAGCCAGTTCGGGGTGTGCGGTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 6440
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 6441 CTGAAGTGCAGGTCTGCTGCCAACCCGACGTGGGGCTGCTCGTGGCTCTCTCCAGCG 6500
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 6501 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 6560
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QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 6561 GCGGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGACACCTTCGTCTC 6620
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 6621 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCCTCGCGCCCTGAGCAAC 6680
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 6681 TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCCTGCCAGCGAAGCCACGACG 6740
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 6741 CCAGCGCGCGACCAACACCGCGGCCACCATCGCTCGCAGCCCTGTCTCCCTGCGC 6800
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuaspPheAla 180
Db 6801 CCAGAGCGGTGCGCGCCAGCGCGGGCGCGAGTGCACACGAGGGGGTGGACTTCGCC 6860
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 6861 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCTG 6920
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 6921 GTTATCACCCCTTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCC 6974

RESULT 15
US-10-723-860-5746
; Sequence 5746, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5746
; LENGTH: 2134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-5746

Alignment Scores:
Pred. No.: 5.17e-114 Length: 2134
Score: 1149.50 Matches: 219
Percent Similarity: 93.2% Conservative: 0
Best Local Similarity: 93.2% Mismatches: 1
Query Match: 92.2% Indels: 15
DB: 9 Gaps: 1

US-10-804-763-1 (1-235) x US-10-723-860-5746 (1-2134)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTGCGGTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTCTGCTGCCAACCCGACGTGGGGTGTCTCGTGGCTCTCTCCAGCGC 299
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Qy      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProIysAla  80
Db      300  CGCGCGCGCGCGCAGTCCACCTTCCTCCTATACCTCTCCCAAAACAAGCCCAAGGCG  359

Qy      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu  100
Db      360  GCCGAGGGGCTGGAC-----  374

Qy     101  ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn  120
Db     375  ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC  434

Qy     121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr  140
Db     435  TCCATCATGTACTTCAGCCACTTCGTGCGGCTCTCTCTGCCAGCGAAGCCACCACGACG  494

Qy     141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg  160
Db     495  CCAGCGCGCGACCAACACCGCGGCCCCACCATCGCGTCCGAGCCCTGTCCCTGGCG  554

Qy     161  ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla  180
Db     555  CCAGAGGCGTCCCGGCCAGCGCGGGGGCGGAGTGACACAGAGGGGCTGGACTTCGCC  614

Qy     181  CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu  200
Db     615  TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTCTCTCTGTCACTG  674

Qy     201  ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro  220
Db     675  GTTATCACCCCTTACTTGCAACACAGGAACCGAAGACGTGTTGCAAAATGTCCTCCGCGCCT  734

Qy     221  ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal  235
Db     735  GTGGTCAAAATCGGAGACAAAGCCCTTTTCGGCGAGATACGTC  779
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Search completed: May 30, 2006, 07:32:02
Job time : 1323.82 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:15:35 ; Search time 23.3372 Seconds
(without alignments)
1705.079 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVKSGDKPSLSARYV 235

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abs806p
-USER=US10804763 @CEN1.1.39 @runat_26052006_165105_14645 -NCPU=6 -ICPU=3
-NO_WRAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
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| 1 | 1247 | 100.0 | 2261 | US-10-511-937-415 |
| 2 | 139 | 11.1 | 1912 | US-11-293-697-1818 |
| 3 | 122 | 9.8 | 944 | US-11-293-697-1585 |
| 4 | 121.5 | 9.7 | 2081 | US-11-293-697-2348 |
| 5 | 120 | 9.6 | 720 | US-11-211-917-39 |
| 6 | 118 | 9.5 | 337 | US-11-211-917-35 |
| 7 | 117 | 9.4 | 707 | US-10-503-433B-19 |
| 8 | 115 | 9.2 | 720 | US-11-211-917-7 |
| 9 | 114 | 9.1 | 720 | US-11-211-917-15 |

| | | | | | | |
|----|-------|-----|------|---|--------------------|---------------------|
| 10 | 113 | 9.1 | 336 | 7 | US-11-211-917-3 | Sequence 3, Appl |
| 11 | 113 | 9.1 | 720 | 7 | US-11-211-917-55 | Sequence 55, Appl |
| 12 | 112 | 9.0 | 336 | 7 | US-11-211-917-11 | Sequence 11, Appl |
| 13 | 112 | 9.0 | 336 | 7 | US-11-211-917-93 | Sequence 93, Appl |
| 14 | 112 | 9.0 | 722 | 6 | US-10-503-433B-22 | Sequence 22, Appl |
| 15 | 112 | 9.0 | 796 | 6 | US-10-503-433B-24 | Sequence 24, Appl |
| 16 | 111.5 | 8.9 | 885 | 7 | US-11-154-103-33 | Sequence 33, Appl |
| 17 | 111 | 8.9 | 337 | 7 | US-11-211-917-51 | Sequence 51, Appl |
| 18 | 110.5 | 8.9 | 792 | 6 | US-10-503-433B-21 | Sequence 21, Appl |
| 19 | 110 | 8.8 | 337 | 7 | US-11-239-308-15 | Sequence 15, Appl |
| 20 | 110 | 8.8 | 704 | 6 | US-10-503-433B-15 | Sequence 15, Appl |
| 21 | 110 | 8.8 | 801 | 6 | US-10-503-433B-14 | Sequence 14, Appl |
| 22 | 109 | 8.7 | 764 | 6 | US-10-503-433B-11 | Sequence 11, Appl |
| 23 | 108 | 8.7 | 720 | 7 | US-11-211-917-31 | Sequence 31, Appl |
| 24 | 108 | 8.7 | 720 | 7 | US-11-211-917-63 | Sequence 63, Appl |
| 25 | 108 | 8.7 | 720 | 7 | US-11-211-917-79 | Sequence 79, Appl |
| 26 | 108 | 8.7 | 720 | 7 | US-11-211-917-101 | Sequence 101, Appl |
| 27 | 108 | 8.7 | 1954 | 7 | US-11-293-697-1648 | Sequence 1648, Appl |
| 28 | 107.5 | 8.6 | 2272 | 6 | US-10-196-749-345 | Sequence 345, Appl |
| c | 107 | 8.6 | 795 | 6 | US-10-503-433B-12 | Sequence 12, Appl |
| 30 | 106 | 8.5 | 336 | 7 | US-11-211-917-27 | Sequence 27, Appl |
| 31 | 106 | 8.5 | 337 | 7 | US-11-211-917-59 | Sequence 59, Appl |
| 32 | 106 | 8.5 | 337 | 7 | US-11-211-917-75 | Sequence 75, Appl |
| 33 | 106 | 8.5 | 608 | 7 | US-11-301-554-908 | Sequence 908, Appl |
| 34 | 106 | 8.5 | 706 | 6 | US-10-503-433B-17 | Sequence 17, Appl |
| 35 | 105.5 | 8.5 | 729 | 7 | US-11-154-103-20 | Sequence 20, Appl |
| 36 | 105.5 | 8.5 | 4027 | 7 | US-11-169-140-1 | Sequence 1, Appl |
| 37 | 105 | 8.4 | 330 | 7 | US-11-254-679-59 | Sequence 59, Appl |
| 38 | 105 | 8.4 | 431 | 1 | US-09-784-950-71 | Sequence 71, Appl |
| 39 | 105 | 8.4 | 732 | 6 | US-10-503-433B-16 | Sequence 16, Appl |
| 40 | 104 | 8.3 | 444 | 1 | US-09-784-950-63 | Sequence 63, Appl |
| c | 104 | 8.3 | 543 | 7 | US-11-301-554-970 | Sequence 970, Appl |
| 42 | 104 | 8.3 | 705 | 7 | US-11-211-917-23 | Sequence 23, Appl |
| 43 | 104 | 8.3 | 803 | 6 | US-10-503-433B-20 | Sequence 20, Appl |
| 44 | 104 | 8.3 | 2598 | 7 | US-11-312-958-31 | Sequence 31, Appl |
| 45 | 103 | 8.3 | 330 | 7 | US-11-254-679-43 | Sequence 43, Appl |

ALIGNMENTS

RESULT 1
US-10-511-937-415
; Sequence 415, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 415
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-415
Alignment Scores:

No - top - best - not - top - best

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Pred. No.: 1,7e-97 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-1 (1-235) x US-10-511-937-415 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACCAGTACCGCCCTTCTCTCGCGTGGCTTCTCTCCAGCGCCGACG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTATCCGGGTGTCGCGCTGGATCGGACCTGGAACTCGGGCGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTCCAAACCCGACGTCGGGCTCTCTGGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCCTC 419
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCCGCGGAGAACGAGGGCTACTATTTCGTCGGCCCTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTGTGCGCGTCTCTCCGACGAGGCCACACAGAG 539
Qy 141 ProAlaProArgProToThrProAlaProThrIleAlaSerGlnProLeuSerIleArg 160
Db 540 CCAGCGCGGACCAACCAACCGCGGCCACCATCGGCTCGGCGCCCTGCTCCCTGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyClyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGCTCCGCGCCAGCGCGGGCGGCGAGTGACACAGAGGGGCTGGACTTCGCC 659
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGTCTCTCTCTGTCACTG 719
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATACCCCTTACTGCAACACAGGAAACGAAAGACGTGTTTGCAAATGTCCCGGCT 779
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 824

RESULT 2
US-11-293-697-1818
; Sequence 1818, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1818
; LENGTH: 1912

US-11-293-697-1818
; Sequence 1585, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1585
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; LENGTH: 944
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-293-697-1585

Alignment Scores:
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 Score: 122.00 Matches: 41
 Percent Similarity: 46.3% Conservative: 15
 Best Local Similarity: 33.9% Mismatches: 51
 Query Match: 9.8% Indels: 14
 DB: 6

US-10-804-763-1 (1-235) x US-11-293-697-1585 (1-944)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAaArg 20
 Db 31 ATGAGGCTCCCT-----GCTCAGCTCTGGGCTGCTAATGCTCTGGGCTCTGGATCC 84
 Qy 21 ProSerGlnPheArgVal-----SerProLeuAspArgThrTrpAsnLeuGluThr 38
 Db 85 AGTGGGGAATATGATGACTCAGCTCCACTCTCCCTGCTCCCGCTCAGCGCTGGAGCGC 144
 Qy 39 ValGluLeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCys 54
 Db 145 GCCTCCATCTCTGCAGTCTAGTCAGAGCTCTGCATAGTATGATGATACACTATG 204
 Qy 55 SerTrpLeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuSer 74
 Db 205 GATTGGTACCTGCAGAGCCAGG-----CAGTCTCCACAGCTCTTGATCTTTTAACT 258
 Qy 75 GlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeu 94
 Db 259 TCTAATCGG-----GCCTCCGGGTC---CCTGACAGGTTCAAGTGGCAGTGATCA 306
 Qy 95 GlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrrPhe 114
 Db 307 GGCACAGATTTATTTCTAAATAATCAGTAGTGAGGCTGAGGATGTTGGGGTTTATTTC 366
 Qy 115 Cys 115
 Db 367 TGC 369

RESULT 4
 US-11-293-697-2348
 ; Sequence 2348, Application US/11293697
 ; Publication No. US20060105376A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/11/293,697
 ; CURRENT FILING DATE: 2005-12-05
 ; PRIOR APPLICATION NUMBER: US/10/108,260
 ; PRIOR FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2348
 ; LENGTH: 2081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-293-697-2348

Alignment Scores:
 Pred. No.: 0.107 Length: 2081
 Score: 121.50 Matches: 67
 Percent Similarity: 32.2% Conservative: 30
 Best Local Similarity: 22.3% Mismatches: 83
 Query Match: 9.7% Indels: 121
 DB: 7

US-10-804-763-1 (1-235) x US-11-293-697-2348 (1-2081)

; LENGTH: 944
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-293-697-1585

Alignment Scores:
 Pred. No.: 0.0343 Length: 944
 Score: 122.00 Matches: 41
 Percent Similarity: 46.3% Conservative: 15
 Best Local Similarity: 33.9% Mismatches: 51
 Query Match: 9.8% Indels: 14
 DB: 6

US-10-804-763-1 (1-235) x US-11-293-697-1585 (1-944)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAaArg 20
 Db 31 ATGAGGCTCCCT-----GCTCAGCTCTGGGCTGCTAATGCTCTGGGCTCTGGATCC 84
 Qy 21 ProSerGlnPheArgVal-----SerProLeuAspArgThrTrpAsnLeuGluThr 38
 Db 85 AGTGGGGAATATGATGACTCAGCTCCACTCTCCCTGCTCCCGCTCAGCGCTGGAGCGC 144
 Qy 39 ValGluLeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCys 54
 Db 145 GCCTCCATCTCTGCAGTCTAGTCAGAGCTCTGCATAGTATGATGATACACTATG 204
 Qy 55 SerTrpLeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuSer 74
 Db 205 GATTGGTACCTGCAGAGCCAGG-----CAGTCTCCACAGCTCTTGATCTTTTAACT 258
 Qy 75 GlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeu 94
 Db 259 TCTAATCGG-----GCCTCCGGGTC---CCTGACAGGTTCAAGTGGCAGTGATCA 306
 Qy 95 GlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrrPhe 114
 Db 307 GGCACAGATTTATTTCTAAATAATCAGTAGTGAGGCTGAGGATGTTGGGGTTTATTTC 366
 Qy 115 Cys 115
 Db 367 TGC 369

RESULT 5
 US-11-211-917-39
 ; Sequence 39, Application US/11211917
 ; Publication No. US20060093600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADUE, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI

```
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-39

Alignment Scores:
Pred. No.: 0.0356 Length: 720
Score: 120.00 Matches: 44
Percent Similarity: 44.1% Conservatives: 16
Best Local Similarity: 32.4% Mismatches: 60
Query Match: 9.6% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-1 (1-235) x US-11-211-917-39 (1-720)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGTCCTCCCTGCTCAGCTCTGGGGCTGTAATGCTCTGGGTCCTGAGTCAGTGGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuLeuGluThrValGlu 40
Db 61 GATATTGATGATCACTCACTCTCCCTGCTCCCTGCGGTCACCCCTGGAGAGCGCGCTCC 120
Qy 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATTCCTCGCAGGCTAGTCAGAGTGTTCTGTATAGTAATGATACAACTATTGGATTGG 180
Qy 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAGCCAGGG-----CAGTCTCCACAGCTCCTGAICTATTGGTTCTAAT 234
Qy 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
Qy 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys--S 116
Db 283 GATTTTACACTGAAATAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGCA 342
Qy 116 erAlaLeuSerAsnSerIleMetTyrPheSerHisPheValPro 130
Db 343 CAAGTTTACAACTCCATT-----CACTTTCCGCCCC 374

RESULT 6
US-11-211-917-35
; Sequence 35, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09

; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09

; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-39

Alignment Scores:
Pred. No.: 0.0356 Length: 720
Score: 120.00 Matches: 44
Percent Similarity: 44.1% Conservatives: 16
Best Local Similarity: 32.4% Mismatches: 60
Query Match: 9.6% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-1 (1-235) x US-11-211-917-39 (1-720)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGTCCTCCCTGCTCAGCTCTGGGGCTGTAATGCTCTGGGTCCTGAGTCAGTGGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuLeuGluThrValGlu 40
Db 61 GATATTGATGATCACTCACTCTCCCTGCTCCCTGCGGTCACCCCTGGAGAGCGCGCTCC 120
Qy 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATTCCTCGCAGGCTAGTCAGAGTGTTCTGTATAGTAATGATACAACTATTGGATTGG 180
Qy 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAGCCAGGG-----CAGTCTCCACAGCTCCTGAICTATTGGTTCTAAT 234
Qy 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
Qy 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys--S 116
Db 283 GATTTTACACTGAAATAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGCA 342
Qy 116 erAlaLeuSerAsnSerIleMetTyrPheSerHisPheValPro 130
Db 343 CAAGTTTACAACTCCATT-----CACTTTCCGCCCC 374

RESULT 7
US-10-503-433B-19
; Sequence 19, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 19
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-4
US-10-503-433B-19

Alignment Scores:
Pred. No.: 0.0627 Length: 707
Score: 117.00 Matches: 29
Percent Similarity: 50.0% Conservatives: 17
Best Local Similarity: 31.5% Mismatches: 38
Query Match: 9.4% Indels: 8
DB: 6 Gaps: 3

; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-35

Alignment Scores:
Pred. No.: 0.0195 Length: 337
Score: 118.00 Matches: 39
Percent Similarity: 46.4% Conservatives: 12
Best Local Similarity: 35.5% Mismatches: 43
Query Match: 9.5% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-1 (1-235) x US-11-211-917-35 (1-337)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTGCGGCTCACCCCTGGAGAGCGGCTCCATCTCCTGCGAGTCTAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGTGTTCTGTATAGTAATGATACAACTATTGGATTGGTACCTGCAGAGCCAGGG 138
Qy 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGTCTTAATCGG-----GCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCys--SerAlaLeuSerAsnSerI 122
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCAATGCAAGTTTACAAACTCCA 300
Qy 122 leMetTyrPheSerHisPheValPro 130
Db 301 TT-----CACTTTCCGCCCC 314
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US-10-804-763-1 (1-235) x US-10-503-433B-19 (1-707)
QY 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 439 GGGCAGAGGTCACCATCTCTGCACTGGAGCAGCTCCAAATCGGGCAGCATGAT 498
QY 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db 499 GTACACTGTATCAGCAGCTCCAGGAGCGGC-----CCCAAACTCCTCATCTATGTT 552
QY 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 553 AACAAATCGGCCCTCAGGGGTC-----CCTGACCGAATCTCTGGCTCCAAG 600
QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyr 113
Db 601 TCTGGACCTCAGCTCCCTGCCATCAGTGGGCTCCGTCGAGGATGAGGCTGATAT 660
QY 114 PheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 661 TACTGTGGGCTCTTGATGACACTGTAAAGTGTATC 696

RESULT 8
US-11-211-917-7
; Sequence 7, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PE/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-7
Alignment Scores:
Pred. No.: 0.095 Length: 720
Score: 115.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.2% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-7 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTGCAGGTCTAGTCAGAGCCCTCTTGATAGTAAATGGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAGAGCCAGGG-----CAGTCTCCACAGCTCCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC-----CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAAATCAGCAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGC 339

RESULT 10
US-11-211-917-3
; Sequence 3, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PE/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-3
Alignment Scores:
Pred. No.: 0.116 Length: 720
Score: 114.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-15 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTGCAGGTCTAGTCAGAGCCCTCTTGATAGTAAATGGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAGAGCCAGGG-----CAGTCTCCACAGCTCCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC-----CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAAATCAGCAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGC 339
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; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-3

Alignment Scores:
Pred. No.: 0.0518 Length: 336
Score: 113.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-3 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCACTCTCTGAGGCTAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCTCTTGATAGTAATAGTACAACTTTTGGATGTTGTTTACCTGCAGAGCGG 138
Qy 63 AlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGTTGGTTCTTAATCGG-----GCCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC-----CCTGACAGGTTTCTAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgGluAsnGluGlyTyTrpPheCys 115
Db 241 AGCAGATTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 11
US-11-211-917-55
; Sequence 55, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-55

Alignment Scores:
Pred. No.: 0.141 Length: 720
Score: 113.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-55 (1-720)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTGGGGCTGTATAGTCTCTGGGTCTCTGGATCCAGTGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGCGCTCC 120
Qy 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCCTCGAGGCTAGTGCAGAGCCTCTGTATAGTAAATGATATAACTATTGATTGG 180
Qy 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsn 76
Db 181 TACCTGCAGAGCCAGG-----CAGTCTCCACACTCTCTGATCTATTGTTGGTTCTAAT 234
Qy 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC---CCTGACAGGTTTCTAGTGGCAGTGGTTTCAGGCACT 282
Qy 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGC 339

RESULT 12
US-11-211-917-11
; Sequence 11, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-11

Alignment Scores:
Pred. No.: 0.063 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 9.0% Indels: 10
DB: 7 Gaps: 4
```

```
US-10-804-763-1 (1-235) x US-11-211-917-11 (1-336)
QY 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCCCTGCAGGCTAGT 78
QY 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCTCTTGATAGTAATGATACAACTTTTGGATTGGTACCTGCAGAGCCAGCG 138
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 103 SerAspPheArgArgGluAsnGluGlyTyTyTyPheCys 115
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 13
US-11-211-917-93
; Sequence 93, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PE/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 93
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-93

Alignment Scores:
Pred. No.: 0.063 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 9.0% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-93 (1-336)
QY 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCCCTGCAGGCTAGT 78
QY 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCTCTTGATAGTAATGATACAACTTTTGGATTGGTACCTGCAGAGCCAGCG 138
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 103 SerAspPheArgArgGluAsnGluGlyTyTyTyPheCys 115
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 14
US-10-503-433B-22
; Sequence 22, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 22
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-20
US-10-503-433B-22

Alignment Scores:
Pred. No.: 0.172 Length: 722
Score: 112.00 Matches: 30
Percent Similarity: 48.3% Conservative: 13
Best Local Similarity: 33.7% Mismatches: 38
Query Match: 9.0% Indels: 8
DB: 3 Gaps: 3

US-10-804-763-1 (1-235) x US-10-503-433B-22 (1-722)
QY 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 438 GGGCAGAGGGTCCACCATCTCTTGCACCTGGGAGCAGCTCCAAACATCGGGGCGTCCGAT 497
QY 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeu 73
Db 498 GTACACTGTATCAGCAGCTCCAGGAGCGGCC-----CCCAAACTCTCTATCTATGGT 551
QY 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 552 AACAACTATCGGCCCTCAGGGGTC-----CCTGACCGATTCTCTGGCTCCAAG 599
QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTy 113
Db 600 TCTGGCACCCTCAGCCTCCCTGGCCATCAGTGGGCTCCGTCGAGGATGAGGCTGATTAT 659
QY 114 PheCysSerAlaLeuSerAsnSerIle 122
Db 660 TACTGTGGCGCTTATGATGACAGTATT 686

RESULT 15
US-10-503-433B-24
; Sequence 24, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:13:46 ; Search time 5108.67 Seconds
(without alignments)
3858.452 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

Scoring table:

| | |
|---------------------------|--|
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| Xgapop 10.0 , Xgapext 0.5 | |
| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNIT=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US10804763@CN 1.1.7986 @runat_26052006_165054_14448 -NCFU=6 -ICPU=3
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DBLEXT=7

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9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1222 | 98.0 | 789 | 2 | BI819839 |
| 2 | 1207 | 96.8 | 804 | 2 | BI820808 |
| 3 | 1192 | 95.6 | 882 | 2 | BI820267 |
| 4 | 1176 | 94.3 | 780 | 2 | BI760947 |

ALIGNMENTS

| | | | | | | |
|------------|---|---|--------|------|--------|-----------------|
| RESULT 1 | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5', | 789 bp | mRNA | linear | EST 04-OCT-2001 |
| LOCUS | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5', | | | | |
| DEFINITION | BI819839 | mRNA sequence. | | | | |
| ACCESSION | BI819839 | GI:15931389 | | | | |
| VERSION | BI819839.1 | GI:15931389 | | | | |
| KEYWORDS | EST. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 | (bases 1 to 789) | | | | |
| AUTHORS | NIH-MGC | http://mgc.ncbi.nlm.nih.gov/. | | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | | |
| JOURNAL | Unpublished (1999) | | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11454 row: d column: 18 High quality sequence stop: 788. | | | | | |

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FEATURES
    source      Location/Qualifiers
1..789
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5182049"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_115"
    /note="Organ: pooled brain, lung, testis; Vector:
    pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of 6 male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1.29e-96      Length:      789
Score:          1222.00      Matches:    234
Percent Similarity: 99.2%      Conservative: 0
Best Local Similarity: 99.2%      Mismatches: 1
Query Match:    98.0%      Indels:     1
DB:             2          Gaps:         0

US-10-804-763-1 (1-235) x B1819839 (1-789)

Qy      1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      76 ATGGCTTACAGTACCGCTTGTCTCGCGTGGCTTGTCTCCAGCGCCAGG 135

Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      136 CCGAGCCAGTTCCGGGTTCGCGCTGATCGGACCTGGAACCTGGCGAGACAGTGGAG 195

Qy      41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      196 CTGAAGTCCAGGTGCTCTGTCCAAACCGACGTCGGGCTGCTGTCTTCAGCGC 255

Qy      61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProIysAla 80
Db      256 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAACAGCCCAAGGCG 315

Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      316 GCCGAGGGGGTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTGTCTCTC 375

Qy      101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      376 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 435

Qy      121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      436 TCCATCATGTACTTCAGCCACTTCGCGCGGTCTTCCTGCCAGCAAGCCACACAGCAGC 495

Qy      141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      496 CCAGCGCGCGGACCAACACCGGCGCCACCATCGGTCCGAGCCCTGTCTCTCGCGC 555

Qy      161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThr-ArgGlyLeuAspPheAl 180
Db      556 CCAGAGGCGTGC CGGCCAGCGCGGGGCGCGAGTGCACACGAGGGGGCTGGAATTCCGC 615

Qy      180 aCysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerIle 200
Db      616 CTGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCCTCTGCACT 675

Qy      200 uValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPr 220
Db      676 GGTATATACCTTTACTCTCAACCAACAGGAACCGAAGAGCGTGTTCGCAAAATGTCCCCCGCC 735

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Qy      220 oValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db      736 TGTGTCAAATCGGGAGACAGCCCGCCTTTCGGCGGAGATACGTC 781

RESULT 2
B1820808
LOCUS      B1820808      804 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION      603034019P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
mRNA sequence.
ACCESSION      B1820808
VERSION      B1820808.1 GI:15932358
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11436 row: e column: 06
High quality sequence stop: 802.

FEATURES
    source      Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5175149"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_115"
    /note="Organ: pooled brain, lung, testis; Vector:
    pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of 6 male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      2.73e-95      Length:      804
Score:          1207.00      Matches:    228
Percent Similarity: 97.9%      Conservative: 0
Best Local Similarity: 97.9%      Mismatches: 5
Query Match:    96.8%      Indels:     0
DB:             2          Gaps:         0

US-10-804-763-1 (1-235) x B1820808 (1-804)

Qy      3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSer 22
Db      7 TTACAGTACCGGCTTGTCTCGCGTGGCTTGTCTCCAGCGCGGCGGAGC 66

Qy      23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db      67 CAGTTCGGGGTGTGCGCCCTGGATCGGACCTGGAACTGGGGGAGACAGTGGAGCTGAAG 126

Qy      43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62

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Db      127  TGCCAGGTGCTGCTGCTCCAAACCGACGTCGGGCTGCTGCTGCTCTTCCAGCGCGCGC 186
Qy      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAaSerProLysAlaAlaGlu 82
Db      187  GCGCGCGCCAGTCCCACTTCTCTATACCTTCTCCAAAACAGCCCAAGCGCGCGAG 246
Qy      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      247  GGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGGACACCTTCGCTCCTCACCTG 306
Qy      103  SerAspPheArgArgGluLeuGlyTyrTyrPheCysSerAlaLeuSerLeuSerLeu 122
Db      307  ACGCACTTCGCGGAGAACGAGGGCTACTATTCTGCTGGCCCTGAGCAACTCCATC 366
Qy      123  MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db      367  ATGTACTTCAGCACCTTCGTGCGGTCTTCCTGCCAGCGAAGCCACACGAGCGCG 426
Qy      143  ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db      427  CGCGGACCAACACCGCGGCCACCATCGGCTGCGAGCCCTGTCTCCCTGGCGCCAG 486
Qy      163  AlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCys 182
Db      487  GGTGCGCGCCAGCGCGCGGGCGCGAGTGCACACGAGGGGCTGGACTTCGCCTGT 546
Qy      183  IleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeuValIle 202
Db      547  ATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTGCTGTTAT 606
Qy      203  ThrLeuTyrCysAaHisArgAaSerLeuArgArgGValCysLysCysProArgPro 222
Db      607  ACCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCATAATGTCCCGGCT 666
Qy      223  LysSerGlyAspLysProSerLeuSerAlaAaTyrVal 235
Db      667  AAATCGGGAGAACGCCAGCCCTTTTCGGCGAGATACGTC 705

RESULT 3
LOCUS   BI820267
DEFINITION BI820267 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:517785 5',
mRNA sequence.
ACCESSION BI820267
VERSION   BI820267.1 GI:15931817
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLNL1443 row: 9 column: 06
High quality sequence stop: 769.
FEATURES
Location/Qualifiers
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:517785"
/lab_host="DH10B"

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/clone lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 6,37e-94 Length: 882
Score: 1192.00 Matches: 231
Percent Similarity: 98.3% Conservatives: 1
Best Local Similarity: 97.9% Mismatches: 1
Query Match: 95.6% Indels: 3
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x BI820267 (1-882)
Qy      3  LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSer 22
Db      65  ATACCAAGTACCGCCTTGTCTGCGCTGGCTTGTCTCCACGCCCGCAGCGCGAGC 124
Qy      23  GlnPheArgValSerProLeuAspArgThrTyrPheLeuGlyValGluThrValGluLeu 42
Db      125  CAGTTCCGGGTGTCCCGCTGGACTCGAACCTGGGGGAGACAGTGGAGCTGAAG 184
Qy      43  CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrLeuPheGlnProArgGly 62
Db      185  TGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGCTGCTCTTCCAGCGCGCGC 244
Qy      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAaSerProLysAlaAlaGlu 82
Db      245  GCGCGCGCGAGTCCCACTTCTCTATACCTTCTCCAAAACAGCCCAAGCGCGCGAG 304
Qy      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      305  GGGCTGGACACCCAGCGGTCTCGGGGAGAGAGTTGGGGGACACCTTCTCTCACCTG 364
Qy      103  SerAspPheArgArgGluAsnGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db      365  AGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCATC 424
Qy      123  MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db      425  ATGTACTTCAGCACTTCGTGCGGTCTTCTCCAGCGAAGCCACACCGCGCGAG 484
Qy      143  ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db      485  CGCGACCAACACCGCGGCCACCATCGGCTGCGAGCCCTGTCTCTGCGCCAGAG 544
Qy      163  AlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCys 182
Db      545  GGTGCGCGCCAGCGCGGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCTGTGAT 604
Qy      183  IleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuVal 202
Db      605  ATCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTGCTGTTAT 664
Qy      202  eThrLeuTyrCysAaHisArgAaSerLeuArgArgValCysLysCysProArgProVal 222
Db      665  CACCCTTTACTGCAACACGAGAACCGAGAGCTGTTTGCATAATGTCCCGGCTGTGT 724
Qy      222  LysSerGlyAspLysProSerLeuSerAlaAaTyrVal 235
Db      725  CAATTCGGGGAGACAATGCCCGAGCTTTCGGCGAGATACGTC 766

RESULT 4
BI760947

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LOCUS      B1760947              780 bp      mRNA      linear      EST 25-SEP-2001
DEFINITION 60304315f1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
mRNA sequence.
ACCESSION  B1760947
VERSION    B1760947.1 GI:15752525
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 780)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM11458 row: e column: 13
            High quality sequence start: 4
            High quality sequence stop: 756.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5183604"
                     /lab_host="DH10B"
                     /clone_lib="NIH MGC 116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female. Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon cloning). Average insert size 1.4 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber (Invitrogen). Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      1.36e-92      Length:      780
Score:          1176.00      Matches:    233
Percent Similarity: 98.3%      Conservative: 0
Best Local Similarity: 98.3%      Mismatches: 1
Query Match:    94.3%      Indels:     4
DB:             2           Gaps:       0

US-10-804-763-1 (1-235) x B1760947 (1-780)

Qy      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      67  ATGGCTTACCAGTGACCGCTTGTCTCGCGTGGCTTGTCTCTCCAGCCCGCAGG 126
Qy      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      127  CCGAGCAGGTTCGGGGTGTGCGCGTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 186
Qy      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      187  CTGAAGTCCAGGTGCTGCTGTCCAACCGCAGCTGGGGTGTGCTGTGCTCTTCCAGCG 246
Qy      61  ArgGlyAlaAlaAsnProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db      247  CGCGGGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 306

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Qy      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      307  GCCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGAGACACCTTCGTCCTC 366
Qy      101  ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db      367  ACCCTGAGCGCACTTCCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 426
Qy      121  SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      427  TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCCTGCCAGCGAAGCCACCAAGAGG 486
Qy      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      487  CCAGCGCGGACACCAACACACCGCGGCCACCACTCGCGTGGCAGCCCTGTCCCTGGCGC 546
Qy      161  ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db      547  CCAGAGCGGTGCCCGCGCAGCGCGGGCGGCGCAGTGACACGAGGGGCTGGACTTCGCC 606
Qy      181  CysAspIleTyTrpIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSer-Le 200
Db      607  TGTGATATCTACATCTGGGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTCTGTCACTT 666
Qy      200  uValIleThr-LeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgP 220
Db      667  GGTATATCACCCCTTTACTCAACCAACAGAACCCGAGACGTGTGTTCGAA-TGTCCCGCGC 725
Qy      220  roValValLysSerGlyAspLysProSerLeu-SerAlaArgTyTr 234
Db      726  CTGTGGTCAAATCGGAGACAAGCCAGCCCTTTTCGGCGGAGATAC 770

RESULT 5
LOCUS      DA931234
DEFINITION DA931234 SPLEN1 Homo sapiens cDNA clone SPLN1000141 5', mRNA
sequence.
ACCESSION  DA931234
VERSION    DA931234.1 GI:82056788
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 838)
            Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
            Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
            Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Koshida,N.,
            Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
            Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
            Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
            Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
            Genome Res. 16 (1), 55-65 (2006)
            16344560
            Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
FEATURES             Location/Qualifiers
     source           1..838

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN1000141"
/issue_type="spleen"
/clone_lib="SPLEN1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 6,15e-92 Length: 838
Score: 1169.00 Matches: 226
Percent Similarity: 98.3% Conservative: 1
Best Local Similarity: 97.8% Mismatches: 4
Query Match: 93.7% Indels: 1
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x DA931234 (1-838)

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QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 89 ATGGCCTTACCAAGTACCGCTTGTCTCCGCTGGCTTGTCTCCACGCCGCGCAGG 148
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 149 CCGAGCCAGTTCGGGTGTGGCGGTGGATCGGACCTGGAACCTGGGCGGAGACAGTGGAG 208
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 209 CTGAAGTGCAGGTGCTGTCTCCACCCGACGTGGGTGCTGTGGTCTTCTCCAGCGC 268
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 269 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACCAAGCCCAAGCG 328
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 329 GCCGAGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTGGGGACACCTTCGTCTCTC 388
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 389 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTGGCCCTTGAGCAAC 448
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 449 TCCATCATGTACTTCAGCCACTTCGTCGGCTCTCTCCAGCGAAGCCACACGACG 508
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 509 CAGCGCGCGCGACCAACACCGCGGCCACCATCGCGTCCGACGCTGTCTCTCTGCGC 568
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisArgGlyLeuAspPheAla 180
Db 569 CCAGAGGCTGCGCGCCAGCGCGGGGGCGGAGTGCACACGAGGGGTGACTTCGCGC 628
QY 181 CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 629 TGTGATATCTACATCTGGGCGCGCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCAC 688
QY 201 ValIleThrLeuTyCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 689 GGTATCACCCCTTTACTGNAACCTACAGAACCCAGACGCTGTTGCAAAATGTCCCGG-CCT 747
QY 221 ValValLysSerGlyAspLysProSerLeuSer 231
Db 748 GTGGTCNAATCGGAGACAAGCCCGACCTTCG 780
```

RESULT 6
CO646993

LOCUS

DEFINITION ILLUMIGEN_MCO_39909 katze_MMPB2 Macaca mulatta cDNA clone
IB10W:22761 5'-similar to Bases 4 to 915 highly similar to human
CD8A (Hs.85258), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISMCO646993
CO646993.1 GI:50568487EST
Macaca mulatta (rhesus monkey)
Macaca mulatta
Macaca mulattaEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE

AUTHORS

Magnes, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., and
Iadonato, S.P.Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human

JOURNAL

PUBMED

COMMENT

15998449
Contact: C. Magnes
Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagnes@illumigen.com

Sequenced on 2004.05.27. 648 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see

http://www.macaque.org

PCR Primers

FORWARD: CCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGCGAATTGGTA

Insert Length: 949 Std Error: 0.00

Plate: CL000326 row: D column: 02

Seq primer: CCTCACTAAAGGGAACAAA

POLYA=No.

FEATURES

source

1..949
/organism="Macaca mulatta"
/mol_type="mRNA"
/strains="Indian"
/db_xref="taxon:9544"
/clone="IB10W:22761"
/sex="male"
/tissue_type="blood"
/cell_type="PBMC"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMPB2"
/note="Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I;
Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.: 9.5e-88 Length: 949
Score: 1122.00 Matches: 216
Percent Similarity: 93.2% Conservative: 5
Best Local Similarity: 91.1% Mismatches: 14
Query Match: 90.0% Indels: 2
DB: 8 Gaps: 0

US-10-804-763-1 (1-235) x CO646993 (1-949)

```
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 56 ATGGCCCTCCCGTGAACGCTTGTCTCTGCGCTGGTCTGTCTCCACGCCGCGCAGG 115
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 116 CCACACCAAGTCCGAGTGTGCGCGCTGGTCCGACCTGGGAGACGCTGGAG 175
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 176 CTGAAGTCCAGGTCTGTCTGTCACACCGACGCTCGGGCTGCTCGTGGTCTTCCAGCGC 235
```

```
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyriLeuSerGlnAsnLysProLysAla 80
Db 236 GCGGCGACCGCGCGCGCCACCTTCTCTATATACCTCTCCCAAAACAAGCCCAAGCG 295
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 296 GCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGGTGGGGACACCTTCGTCTC 355
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyriTyriPheCysSerAlaLeuSerAsn 120
Db 356 ACCCTAGCTGACTTCCGCGCAAGAGAACGAGGGCTACTATTTCGTCTCGGCCCTGAGCAAC 415
Qy 121 SerileMetTyriPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 416 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACCACTACG 475
Qy 141 ProAlaProArgProProThrProAlaProThrTrileAlaSerGlnProLeuSerLeuArg 160
Db 476 CCAGCGCGCGATCCCCACACCGCGGCCACACCGCGTCCGAGCCCTGTCTCTGCGC 535
Qy 161 ProGluLaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 536 CCAGAGGCGTCCGCGCCAGCGCGGGGCTCAGTGAACACAGAGGGCTGGACTTCGCC 595
Qy 181 CysaspIleTyriLeuTrpAla-ProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLe 200
Db 596 TGTGATATCTACATCTGGGCGCGCCCTTGGCTGGGGCCCTGGCGGGTCTCTTCCTGTCTACT 655
Qy 200 uValIleThrLeuTyriCysAsnHisArgAsnArgArgValCysLys-CysProArgP 220
Db 656 GGGCATCACCTTTACTGCAACACAGAGAACCGAAACGTGTGGCAATTTGTCTCCAGGC 715
Qy 220 roValValLysSerGlyAspLysProSerLeuSerAlaArgTyriVal 235
Db 716 CTGTGTTCAANTCGGAGGCAAGCCCGCTTTCGGAAGATACGTC 762
```

RESULT 7

DN997301

LOCUS

DEFINITION TC111602 Human breast cancer tissue, large insert, pcwv expression library Homo sapiens cDNA clone TC111602 5' similar to Homo sapiens CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 1, mRNA sequence.

ACCESSION

DN997301

DN997301.1

GI:66257128

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 704)

Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,

Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,

Zhang,X., Jay,G. and He,W.

High-throughput cloning of full-length human cDNAs directly from

cDNA libraries optimized for large and rare transcripts

Unpublished (2005)

Contact: Kovacs, KF

High throughput cDNA Cloning

Origene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188

Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length

cloning project at Origene Technologies, Inc.

Please contact Origene for access.

Origene Technologies, Inc.

6 Taft Ct. Suite 100

Rockville, MD 20850

Tel: (301) 340-3188

http://www.origene.com

Seq primer: pcwv6 5prime forward vector primer, OriGene Technologies Inc.

FEATURES

source

1..704

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TC111602"

/tissue_type="Breast cancer"

/clone_lib="Human breast cancer tissue, large insert, pcwv expression library"

/note="Organ: Mammary gland (cancer tissue); Vector: pcwv6-XL5; Site 1: EcoRI; Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Alignment Scores:

Pred. NO.: 5.85e-87 Length: 704

Score: 1111.00 Matches: 210

Percent Similarity: 99.5% Conservative: 0

Best Local Similarity: 99.5% Mismatches: 1

Query Match: 89.1% Indels: 0

DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x DN997301 (1-704)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 70 ATGGCCCTTACAGTGACCGCTTCTCTCGCGTGGCTTGGCTCTCCAGCCGCCAGG 129

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 130 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGACCTGGAACTGGGCGAGACAGTGGAG 189

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 190 CTGAAGTGCCAGGTGCTGTCTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCCAGCGC 249

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyriLeuSerGlnAsnLysProLysAla 80

Db 250 GCGGCGCGCGCGCGCGCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 309

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 310 GCCGAGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCTC 369

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyriTyriPheCysSerAlaLeuSerAsn 120

Db 370 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCGTCTCGGCCCTTGAGCAAC 429

Qy 121 SerileMetTyriPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140

Db 430 TCCATCATGTACTTCAGCCACTTCGTGCGGTTCCTGCCAGCGAAGCCCAAGCGGCG 489

Qy 141 ProAlaProArgProProThrProAlaProThrTrileAlaSerGlnProLeuSerLeuArg 160

Db 490 CCAGCGCGCGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCTCTGCGC 549

Qy 161 ProGluLaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180

Db 550 CCAGAGGCGTCCGCGCCAGCGCGGCGCGAGTGCACACAGGGGGGTGGACTTCGCC 609

Qy 181 CysaspIleTyriLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200

Db 610 TGTGATATCTACATCTGGGCGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCTACTG. 669

Qy 201 ValIleThrLeuTyriCysAsnHisArgAsnArg 211

Db 670 GTTATCACCTTTTACTGCAACACACAGGAACCGA 702

```

RESULT 8
BI911195
LOCUS 603062918F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211989 5',
DEFINITION mRNA sequence.
ACCESSION BI911195
VERSION BI911195.1 GI:16174808
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 796)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11532 row: d column: 06
High quality sequence start: 29
High quality sequence stop: 791.
FEATURES
source
1..796
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5211989"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
(note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library.")
ORIGIN
Alignment Scores:
Pred. No.: 3.89e-85 Length: 796
Score: 1091.00 Matches: 217
Percent Similarity: 98.2% Conservative: 0
Best Local Similarity: 98.2% Mismatches: 1
Query Match: 87.5% Indels: 4
DB: 2 Gaps: 0
US-10-804-763-1 (1-235) x BI911195 (1-796)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 140 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCCTTGCTGCTCCACGCCGCGCAGG 199
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGlnThrValGlu 40
Db 200 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGGACCTGGAACTGGGGGAGACGTGGAG 259
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 260 CTGAAGTCCAGGTCTGCTGCTCCACCCGACGTGGGCTGCTGCTGCTCTTCCAGCGG 319
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

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Db 320 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCAGGCG 379
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyArgLeuGlyAspThrPheValLeu 100
Db 380 GCGGAGGGGCTGACACCCAGCGGTTCGGGCAAGAGGTGGGGACACCTTCGTCCTC 439
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 440 ACCCTGAGCGACTTCGCCCGAGAGAACGAGGGCTACTATTCTTGCTCGGCCCTGAGCAAC 499
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 500 TCATCATGTACTTACGCCACTTCGTGCGGCTTCTCTCCAGCAAGCCACGACG 559
QY 141 ProAlaProArgProProThrProAla-ProThrIleAlaSerGlnProLeuSerLeuAr 160
Db 560 CCAGGCCCGGACCAACACCGCTGCCACCATCGCGTGCAGCCCCCTGTCCTGCG 619
QY 160 gProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAl 180
Db 620 CCCAGAGGGCTGCCGCCAGCGCGCGGCGCAGTGCACACGAGGGGCTGCACCTCGC 679
QY 180 a-CysAspIleTyrIleTrpAlaProLeuAla-GlyThrCysGlyValLeuLeuSer 199
Db 680 CCGTGATATCTACATCTGGCGGCCCTTGGCCCGGACTTGTGGGTCTCTTCTCTGTC 739
QY 200 LeuValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 740 CTGGTTATCACCTTTACTGT-AACCACAGAAACCGAAGACGTGTTTGCAATGTCCC 795

```

```

RESULT 9
BI835165
LOCUS 603088746F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5227906 5',
DEFINITION mRNA sequence.
ACCESSION BI835165
VERSION BI835165.1 GI:15946715
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11573 row: k column: 11
High quality sequence stop: 639.
FEATURES
source
1..840
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5227906"
/lab_host="DH10B"
/clone_lib="NIH_MGC_120"
(note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is

```



```

QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 459 TCCATCATGACTTACAGCACTTCGTGCGGCTTCTCTGCCAGCAAGCCACCAAGC 518

QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 519 CCAGCGCGCGGACCAACACCGGCGGCCACCATCGCTCGAGCCCTGTCCCTGCGC 578

QY 161 ProGluAlaCyArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 579 CCAGAGCGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638

QY 181 CysAspIleTyrlleTrrAlaProLeuAla-GlyThrCysGlyValLeu-LeuLeu-Se 199
Db 639 TGTGATATCTACATCTGGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTCGTGC 698

QY 199 rLeuValIleThrLeuTyCysAsnHisArgAsnArgArgVal 214
Db 699 ACTGGTTATCACCTTTACTGCAACCAACAGTAAGTCCCGGAATC 744

RESULT 11
LOCUS DA946587 580 bp mRNA linear EST 03-DEC-2005
DEFINITION DA946587 SPLEN2 Homo sapiens cDNA clone SPLEN2022409 5', mRNA
sequence.
ACCESSION DA946587.1 GI:83054667
VERSION DA946587.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saiko,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES
Location/Qualifiers
1..580
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN2022409"
/tissue_type="spleen"
/clone_lib="SPLEN2"
/note="Vector: pME18SFL3"

ORIGIN
Alignment Scores: 4.73e-78 Length: 580
Pred. No.: 1008.00 Matches: 192
Score: 99.5% Conservative: 1
Percent Similarity:

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```

Best Local Similarity: 99.0% Mismatches: 0
Query Match: 80.8% Indels: 1
DB: Gaps: 0

US-10-804-763-1 (1-235) x DA946587 (1-580)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaArg 20
Db 1 ATGGGCTTACCAGTACCGCCCTTGTCTCTGCGCTGGCCTTGTCTCCACGCGCAGG 60

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGly-GluThrValGI 40
Db 61 CCGAGCCAGTTCGGGGTGTGATCGGATCGGACTGGAACTGGGCTGAGACAGTGA 120

QY 40 uleuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPr 60
Db 121 GTGAAGTGCAGGTGTGCTGCCAACCCGACGTCGGGCTGCTGTGGCTCTTCAGGC 180

QY 60 oArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlleuSerGlnAsnLysProLysAl 80
Db 181 GCGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAGGCCAAGGC 240

QY 80 aAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValle 100
Db 241 GCCCGAGGGGTGGACACCCAGCGTTCCTCGGGCAAGAGGTTGGGGGACACCTTCGTC 300

QY 100 uThrLeuSerAspPheArgGluAsnGluGlyTyrlleuTyrlleuPheCysSerAlaLeuSerAs 120
Db 301 CACCTTGAGGACTTCCCGCGGAGAGAACGAGGGGCTACTATTTCCTCGGCCCTGAGCAA 360

QY 120 nSerIleMetTyrllePheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 CTCATCATGATCTTACAGCCACTTCGTGCGGCTCTCTCTGCGCAGCAAGCCACCAACG 420

QY 140 rProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuAr 160
Db 421 GCCAGCGCGCGGACCAACCAACACCGCGGCCCAACCATCGCGTCGACGCCCTGTCTGCG 480

QY 160 gProGluAlaCyArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAl 180
Db 481 CCCAGAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540

QY 180 aCysAspIleTyrlleTrrAlaProLeuAlaGlyThrCys 193
Db 541 CTGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGT 580

RESULT 12
LOCUS CR619549 1948 bp mRNA linear HTC 21-JUL-2004
DEFINITION CR619549 full-length cDNA clone CS0D1070YG17 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR619549
VERSION CR619549.1 GI:50500356
KEYWORDS HTC; CNSLT.cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1. (bases 1 to 1948)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2. (bases 1 to 1948)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

```


NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

Location/Qualifiers
 source
 1..569
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="THYMU2034397"
 /tissue_type="Thymus"
 /clone_lib="THYMU2"
 /note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:
 Pred. No.: 2,31e-77 Length: 569
 Score: 1000.00 Matches: 188
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 80.2% Indels: 0
 DB: Gaps: 0

US-10-804-763-1 (1-235) x DB124972 (1-569)

Qy 5 ValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSerGlnPhe 24
 Db 2 GTGACCGCGCTTCTCTCGCGCTGGCTTGTCTCCAGCGCGAGCGAGTTC 61
 Qy 25 ArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln 44
 Db 62 CGGGTGTGCGCGCTGGATCGGACCTGGAACTTGGCGGACAGTGGAGCTGAAGTCCAG 121
 Qy 45 ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGlyAlaAla 64
 Db 122 GTGCTGTGTCCAAACCGGCGCTGGCTGTCTTCCAGCGCGCGCGCGCG 181
 Qy 65 AlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAlaAlaGluGlyLeu 84
 Db 182 GCAGTGTCCACCTTCTCTTATACCTTCTCCAAACAAGCCAGCGCGCGCGGGGTG 241
 Qy 85 AspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeuSerAsp 104
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 Qy 105 PheArgArgGluAsnGluGlyTyrlTrpPheCysSerAlaLeuSerAsnSerIleMetTyr 124
 Db 302 TTCCGCGGAGAGACAGAGGGCTACTATTCTCGCGCGCGCTGAGCAACTCCATCATGTAC 361
 Qy 125 PheSerHisPheValProValPheLeuProAlaLysProThrThrProAlaProArg 144
 Db 362 TTCACCGCACTTCGTGCGCGCTCTTCCTGCGAGGAGCCACCCAGCGCGCGCGCA 421
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 Db 422 CCACCAACACCGCGCGCCACCATCGGTGCGAGCCCTTCTCTGGCCCGAGGGGTGC 481
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 Db 542 ATCTGGCGCGCTTGGCGGGGACTTGT 568

RESULT 15
 DA958887
 LOCUS
 DEFINITION
 ACCESSION

DA958887 555 bp mRNA linear EST 11-NOV-2005
 DA958887 SPLEN2 Homo sapiens cDNA clone SPLEN2038708 5', mRNA

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 Db 157 CTGAAGTGCAGGTGCTGTCTCAACCCGACGTCGGGTCTCGTGGCTTCTCCAGCG 216
 Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAla 80
 Db 217 CGCGCGCGCGCGCGCGCTTCTCTCTATACCTCTCCAAACAAGCCAGCGGG 276
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 277 GCCAGGGGCTGACACCCAGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCTGCTC 336
 Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrlTrpPheCysSerAlaLeuSerAsn 120
 Db 337 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGGTACTATTCTGTCTCGCGCTGAGCAAC 396
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
 Db 397 TCCATCATGTACTTCAGCCACTTCTGTGCGCGTCTTCTGCGAGGAAGCCACCGACG 456
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
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 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
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 Qy 181 CysAspIleTyrlTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
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DEFINITION

sequence.

ACCESSION

DB124972

VERSION

DB124972.1 GI:83212682

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kishida,N., Yonoyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

JOURNAL

16344560

PUBLISHED

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamstari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

COMMENT

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VERSION DA958887.1 GI:82064474
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1. (bases 1 to 555)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Teuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Sugano,S.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Isogai,S.
TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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ORIGIN

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Query Match: 78.8% Indels: 0
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US-10-804-763-1 (1-235) x DA958887 (1-555)

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Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
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Qy 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 183 TCCCAAAACAGCCCAAGCGCGCGCGCGCGCGCGCTGGACACCCAGCGTTTCTCGGCAAGAGG 242
Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyr 113
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Job time : 5113.67 secs

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Db 363 CCAGCGAAGCCACACGACGCGCGCGGACCAACACCGCGCGCCACCATCGGG 422
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Db 423 TCGCAGCCCTGTCCCTGCGCCAGAGCGCTGCCGCGCGCGCGCGCGCGCGCGCGAGTGCAC 482
Qy 174 ThrArgGlyLeuAspPheAlaCysAspIleTyrIleTTPAlaProLeuAlaGlyThrCys 193
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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(without alignments)
11658.210 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb_pat.*
- 3: gb_ph.*
- 4: gb_pl.*
- 5: gb_pr.*
- 6: gb_ro.*
- 7: gb_sts.*
- 8: gb_sy.*
- 9: gb_un.*
- 10: gb_vi.*
- 11: gb_ov.*
- 12: gb_hcg.*
- 13: gb_in.*
- 14: gb_om.*
- 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 21 | 708 | 31.3 | 708 | 2 | AX764523 | Sequence |
| 22 | 704.8 | 31.2 | 708 | 2 | AX764527 | Sequence |
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| 24 | 692 | 30.6 | 1995 | 2 | DD211086 | TRANSGENI |
| 25 | 690 | 30.5 | 690 | 2 | DD211090 | TRANSGENI |
| 26 | 690 | 30.5 | 2411 | 2 | DD211089 | TRANSGENI |
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| 28 | 689.4 | 30.5 | 8858 | 2 | DD211083 | TRANSGENI |
| 29 | 689 | 30.5 | 889 | 2 | DD211094 | TRANSGENI |
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| 38 | 610.4 | 27.0 | 708 | 5 | SSC130818 | Sequence |
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| 45 | 507 | 22.4 | 552 | 2 | CQ462237 | Sequence |

ALIGNMENTS

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DEFINITION Sequence 2 from Patent WO2004083404.
ACCESSION CQ882010
VERSION CQ882010.1 GI:54034736
KEYWORDS
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Qi, Y., Zhang, X. and Konigsberg, P.J.
TITLE Gene therapy vectors having reduced immunogenicity
JOURNAL Patent: WO 2004083404-A 2 30-SEP-2004;
Isogenis, Inc. (US)
FEATURES
Location/Qualifiers
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| 1261 | Db | GCTCAGGGCTCTTTCTCTCCACACCAATTCAGGTCTTCTTCTTCGAGGCCCCCTGTCTCAGGG | 1322 |
| 1321 | Qy | TGAGGTGCTTTGAGTCTCCAAACGGCAAGGAAACAAGTACTTCTTTGATACCTGGGATACTGT | 1380 |
| 1321 | Db | TGAGGTGCTTTGAGTCTCCAAACGGCAAGGAAACAAGTACTTCTTTGATACCTGGGATACTGT | 1380 |
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| 1501 | Qy | AATAAAATGAAGTGGTGAGCTTAAACCTCGAAAAATGAATCCCTCTATCTCTAAAGAAAAAT | 1560 |
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| 1921 | Qy | GGAGAGAAAAAACCCTTAAGTAGATAAGGAAATAAGAACCACTCATAAATTCCTACCTTAGG | 1980 |
| 1921 | Db | GGAGAGAAAAAACCCTTAAGTAGATAAGGAAATAAGAACCACTCATAAATTCCTACCTTAGG | 1980 |
| 1981 | Qy | AATAATCTCCTGTTAATATGGGTGACATTCCTCTGTATATTTTCTACATACATGTAA | 2040 |
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| 2041 | Qy | AATATGCTTTCTTTTAAATAGGGTTGACTATCTGTTTATGAGTGGCTTTAATGAAT | 2100 |
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| VERSION | | CQ843147.1 | GI:50894934 |
| | | | PAT 02-AUG-2004 |


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RESULT 3
AK124156 3048 bp mRNA linear PRI 20-JAN-2006
LOCUS Homo sapiens cDNA FLJ42162 fis, clone THYMU2005303, highly similar
to T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR.
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ACCESSION AK124156
VERSION AK124156.1 GI:34529876
KEYWORDS oligo capping, fis (full insert sequence).
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SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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REFERENCE 1
AUTHORS Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Negahari, K., Maehno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
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TITLE 2 (bases 1 to 3048)
JOURNAL Isogai, T. and Yamamoto, J.
REFERENCE Direct Submission
```

```
AUTHORS Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute.
TITLE Genomics Laboratory; 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan
JOURNAL (E-mail: flj-cdna@nifty.com, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: Reverse Proteomics Research Institute, HRI and
RAB.
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ORIGIN

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Query Match 94.3%; Score 2132.8; DB 5; Length 3048;
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QY 181 CGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACTTGGAACTTGGGGGAGACAGTGAGC 240
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QY 841 CCATCTACATTACTTCAAACTGAGATCTCTTTTGGGAGGCAAGTCTCTTCCCTTTCAT 900
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| QY | 1021 | AGTACACCAAGGTCACAATACCTGTTGTGGCCACATCGCGTAGGGGTGAAGAGGG | 1080 |
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| QY | 1141 | CAATCTCAACCTTCTCCCGCCGTTTTCACAAAGGGGAGGCTTAAGCCAGAGACAGCT | 1200 |
| Db | 2053 | CGGTCTCAACCTTCTCCCGCCGTTTTCACAAAGGGGAGGCTTAAGCCAGAGACAGCT | 2112 |
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| QY | 1381 | GCCAGAGCTCGAGAGGTAAATGAATTAAGAAGAGACTGCTTGGCAGAGTCTTAT | 1440 |
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| QY | 1621 | CCCATGAAGAGCAGAGGCTACCCCTTTACAATAAGATTTGAGCATCAGTCAGGTTAA | 1680 |
| Db | 2533 | CCCATGAAGAGCAGAGGCTACCCCTTTACAATAAGATTTGAGCATCAGTCAGGTTAA | 2592 |
| QY | 1681 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA | 1740 |
| Db | 2593 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA | 2652 |
| QY | 1741 | CTTTTATATCTTTGTAAGACAATTTGAGAGGCCCTCACACAGCCCTGCGCTCTGCT | 1800 |
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2041 AATATGCTCTTCTTTTAAATAGGTTGCTACTATGCTCTTATGAGTGGCTTTAATGAAT 2100
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| | | | | | |
|------------|--|-------------|------|--------|-----------------|
| RESULT 4 | BC025715 | 2150 bp | mRNA | linear | PRI 29-JUN-2004 |
| LOCUS | Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript variant 1, mRNA (CDNA clone MGC:34614 IMAGE:5227906), complete cds. | | | | |
| DEFINITION | BC025715 | | | | |
| ACCESSION | BC025715.1 | GI:19344021 | | | |
| VERSION | MGC. | | | | |
| KEYWORDS | Homo sapiens (human) | | | | |
| SOURCE | Homo sapiens | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 2150) | | | | |
| AUTHORS | Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wille, K.C., Hale, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalek, U., Smalley, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. | | | | |
| TITLE | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences | | | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | | | | |
| PUBMED | 12477932 | | | | |
| REFERENCE | 2 (bases 1 to 2150) | | | | |
| AUTHORS | Strausberg, R. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | | | | |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov | | | | |
| COMMENT | Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Iaric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgenev, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. | | | | |

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 49 Row: 0 Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 27886641.

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ORIGIN

Query Match 94.1%; Score 2127; DB 5; Length 2150;
Best Local Similarity 99.7%; Pred.No. 0;
Matches 2141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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| Qy | 1261 | GCTCAGGCTCTTTCCTCCACACCATTCAGGTCTTTCTTCGAGGCCCCCTGTCTCAGGG | 1320 |
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| Qy | 1441 | AATGTAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCTAAATTTGTATAGACTTAA | 1500 |
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| Qy | 1501 | AATAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 |
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| Qy | 1561 | CTCTGTGAACCCCTATGTGGAGGCGAATTTGCTCTCCAGCCCTTGCAATTCGAGAGGG | 1620 |
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| Db | 1630 | CTTTTATATCTTTGTAAGACAATTTGTTGGAGAGCCCTCACAAGCCCTGGCCTCTGCT | 1689 |
| Qy | 1801 | CAACTAGCAGATACAGGATGAGGACCTTGACTCTCTTAAGGAGGCTGAGAGCCCAAA | 1860 |
| Db | 1690 | CAACTAGCAGATACAGGATGAGGACCTTGACTCTCTTAAGGAGGCTGAGAGCCCAAA | 1749 |
| Qy | 1861 | CTGCTGCTCCCAACATGCACCTTCTTGTCTTAAGGTATGTTCAAGCAATGCTGCCAAT | 1920 |
| Db | 1750 | CTGCTGCTCCCAACATGCACCTTCTTGTCTTAAGGTATGTTCAAGCAATGCTGCCAAT | 1809 |
| Qy | 1921 | GGAGAGAAAACTTAAGTAGATAGGAATAAGAACCACTCATTAATTTCTTCCACTTAGG | 1980 |
| Db | 1810 | GGAGAGAAAACTTAAGTAGATAGGAATAAGAACCACTCATTAATTTCTTCCACTTAGG | 1869 |
| Qy | 1981 | AATAATCTCTCTGTTAATATGTTGATACATTTCTCTGATTATTTCTACACATACATGTA | 2040 |
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| Qy | 2041 | AATATGCTCTTTCTTTTAAATPAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAAT | 2100 |
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| | | | | | |
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| RESULT 6 | AK097942 | 2090 bp | mRNA | linear | PRI 20-JAN-2006 |
| LOCUS | Homo sapiens CDNA FLJ40623 fis, clone THYMU2013863, highly similar to T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR. | | | | |
| DEFINITION | AK097942 | | | | |
| ACCESSION | AK097942.1 | GI:21757848 | | | |
| VERSION | | | | | |
| KEYWORDS | oligo capping; fis (full insert sequence). | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | | | | | |
| AUTHORS | Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ichii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosokiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirao, K., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yoshida, M., Hoto, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T. O., Nomura, Y., Toiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Saeki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shiohara, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, H., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Maehuo, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara O., Isogai, T. and Sugano, S. | | | | |
| TITLE | Complete sequencing and characterization of 21,243 full-length human cDNAs | | | | |
| JOURNAL | Nat. Genet. 36 (1), 40-45 (2004) | | | | |
| PUBMED | 14702039 | | | | |
| REFERENCE | | | | | |
| AUTHORS | Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Maehuo, Y., Nagai, K. and Isogai, T. | | | | |
| TITLE | NEDO human cDNA sequencing project | | | | |
| JOURNAL | Unpublished | | | | |
| REFERENCE | 3 (bases 1 to 2090) | | | | |
| AUTHORS | Isogai, T. and Yamamoto, J. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu Chiba 292-0812, Japan (E-mail: filj-cdn@nifty.com, tel:81-438-52-3975, Fax:81-438-52-3986) | | | | |
| COMMENT | NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB. | | | | |
| FEATURES | Location/Qualifiers | | | | |
| Source | 1. .2090 | | | | |

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RESULT 7
HUMTCXAAA
LOCUS HUMTCXAAA 1975 bp mRNA linear PRI 14-JAN-1995
DEFINITION Human T-cell differentiation antigen Leu-2/T8 mRNA, partial cds.
ACCESSION M12824
VERSION M12824.1 GI:339426
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
REFERENCE 1 (bases 1 to 1975)
AUTHORS Sukhatme,V.P., Sizer,K.C., Vollmer,A.C., Hunkapiller,T. and
Parnes,J.R.
TITLE The T cell differentiation antigen Leu-2/T8 is homologous to
immunoglobulin and T cell receptor variable regions
JOURNAL Cell 40 (3), 591-597 (1985)
PUBMED 3918796
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Db 1801 ACTCTCTTAAGAGGCTGAGAGGCCAACTGCTGTCTCCAAACATGCACTTCTCTGTTAA 1860
QY 1893 GGTATGTTACAGCAATGCTGCCATTCGAGAGGAAACCTTAAGTAGATAGGAAATA 1952
Db 1861 GGTATGTTACAGCAATGCTGCCATTCGAGAGGAAACCTTAAGTAGATAGGAAATA 1920
QY 1953 AGAACCACTCATAATTTCTTCACTTAGGAATAATCTCTGTTAAATATGTTGTACA 2007
Db 1921 AGAACCACTCATAATTTCTTCACTTAGGAATAATCTCTGTTAAATATGTTGTACA 1975

RESULT 8

AC064848
LOCUS AC064848 135809 bp DNA linear PRI 15-APR-2005
DEFINITION Homo sapiens BAC clone RP11-81F3 from 2, complete sequence.
ACCESSION AC064848
VERSION AC064848.5 GI:15638742
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 135809)
AUTHORS Kruchowski, S., Haakenson, W. and Boyer, E.
TITLE The sequence of Homo sapiens BAC clone RP11-81F3
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 135809)
AUTHORS Waterston, R.H.

TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (23-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 135809)
Waterston, R.H.
Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 135809)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 135809)
Wilson, R.K.
Direct Submission
Submitted (15-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 18, 2001 this sequence version replaced gi:13592273.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: submissions@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH0081F03

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-269K22, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-81F3; actual end is at base position 34458 of RP11-269K22.

RP11-81F3 from base positions 17803 to 18103 and 101913 to 101968 are represented by sequence derived from PCR.

FEATURES
source

Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-81F3"
/clone_lib="RPCI-11"
576. .806

misc_feature

Db 23614 TATTTCTACATACATGTAATAATGCTTTCTTTTAAATAGGGTTGTACTATGCT 23673

Qy 2079 GTTATGAGTGGCTTTAATGAATAAACAATTGTAGCATCTCTTTAATGGGTAAACAGCA 2137

Db 23674 GTTATGAGTGGCTTTAATGAATAAACAATTGTAGCATCTCTTTAATGGGTAAACAGCA 23732

RESULT 9

HUMCD8A3

LOCUS

DEFINITION Homo sapiens T cell surface glycoprotein (CD8A) gene, exons 5 and 6.

ACCESSION M26315

VERSION M26315.1 GI:341466

KEYWORDS CD8 antigen; T cell surface glycoprotein CD8-alpha; alternative splicing.

SEGMENT 3 of 3

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1729)

AUTHORS Normant, A.M., Lonberg, N., Lacy, E. and Littman, D.R.

TITLE Alternatively spliced mRNA encodes a secreted form of human CD8 alpha. Characterization of the human CD8 alpha gene

JOURNAL J. Immunol. 142 (9), 3312-3319 (1989)

PUBMED 2496167

COMMENT Original source text: Homo sapiens DNA.

FEATURES

Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="2p12"

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join(M26313..1:213..261,M26313..1:356..709,

M26314..1:225..335,M26314..1:542..652,102..132,304..355)

/gene="CD8A"

/codon_start=1

/product="CD8 antigen"

/protein_id="AAA79217.1"

/db_xref="GI:1019167"

/db_xref="GDB:G00-120-581"

/translation="WALPVTALLPLALLHAARPSQFRVSPLDRTWNLGETVELKQ

VLLSPTSGCWLQFPRGAASPTFLYLSONKPKAASGLDQRFSGRLGDTFVLTL

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RPVKSGDKPLSARYV"

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/note="alternatively spliced"

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/translation="WALPVTALLPLALLHAARPSQFRVSPLDRTWNLGETVELKQ

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/number=4

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/gene="CD8A"

/note="G00-120-581"

/number=5

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/gene="CD8A"

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polyA_signal

polyA_signal

ORIGIN

Query Match 60.2%; Score 1361.4; DB 5; Length 1729;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1368; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 759 GTTTCGAATGTCCTCCGGCTGTGCTCAAAATCGGAGACAAGCCAGCCCTTTGGCGAGA 818

Db 287 GCTTTCTCTCTTTTCAGGCTGTGTGTCAAATCGGAGACAAGCCAGCCCTTTGGCGAGA 346

Qy 819 TACGCTTAACCTGTGCAACAGCCACTACATTACTTTCAAACCTGAGATCTCTCTTTTGG 878

Db 347 TACGCTTAACCTGTGCAACAGCCACTACATTACTTTCAAACCTGAGATCTCTCTTTTGG 406

Qy 879 GGAGCAAGTCTTCCCTTTTCATTTTTTCCAGTCTTCTCTCTCTGTGTATTCAATCTCATGA 938

Db 407 GGAGCAAGTCTTCCCTTTTCATTTTTTCCAGTCTTCTCTCTCTGTGTATTCAATCTCATGA 466

Qy 939 TTATTATTTTAGTGGGGGGGGTGGGAAAAGATTACTTTTTCTTTATGTGTGTGACGGGA 998

Db 467 TTATTATTTTAGTGGGGGGGGTGGGAAAAGATTACTTTTTCTTTATGTGTGTGACGGGA 526

Qy 999 AACAAAACTAGTATAAATCTACAGTACACCAAGGGTCAACAATCTGTGTGCGCACAT 1058

Db 527 AACAAAACTAGTATAAATCTACAGTACACCAAGGGTCAACAATCTGTGTGCGCACAT 586

Qy 1059 CGCGTAGGGCGTGGAAAAGGGCCAGGCTACCCGACAGAGTTCTCAGAAATCATGCT 1118

Db 587 CGCGTAGGGCGTGGAAAAGGGCCAGGCTACCCGACAGAGTTCTCAGAAATCATGCT 646

Qy 1119 GAGAGAGCTGGAGGACCCATGCCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGG 1178

Db 647 GAGAGAGCTGGAGGACCCATGCCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGG 706

Qy 1179 AGGCTAAAGCCAGAGACAGCTTGTATCAAAAGGCACACAGAGTTCAGGGTTGAGGAGTA 1238

Db 707 AGGCTAAAGCCAGAGACAGCTTGTATCAAAAGGCACACAGAGTTCAGGGTTGAGGAGTA 766

Qy 1239 GCTGGAGGAGCTTGTCTCCAGCTCAGGGCTCTTTCTCCACACCATTCAGGCTCTTTCT 1298

Db 767 GCTGGAGGAGCTTGTCTCCAGCTCAGGGCTCTTTCTCCACACCATTCAGGCTCTTTCT 826

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Qy 1359 TTCTTGATACCTGGGATCTGTCCCGCAGAGCTCCAGAGGTAATGAATTAAGAGAGA 1418

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Db 947 ACTGCTTTGGCAGAGTTCTATATGTAATAAATAATCAGACTTTTTTTTTTATATCA 1006

Qy 1479 GCCTAAAAATTGTATAGACCTAAAAATAAATGAAGTGTGAGCTTAACCTCGAAATGAA 1538

Db 1007 GCCTAAAAATTGTATAGACCTAAAAATAAATGAAGTGTGAGCTTAACCTCGAAATGAA 1066

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Db 1067 TCCCTCTATCTCTAAAGAAATCTCTGTGAAACCCCTATGTGGAGGGCGGAATTGCTCTCC 1126
Qy 1599 CAGCCCTTGCATTTCAGAGGGGCCCATGAAAGAGAGCAGGCTACCCCTTTTACAAATAGAA 1658
Db 1127 CAGCCCTTGCATTTCAGAGGGGCCCATGAAAGAGAGCAGGCTACCCCTTTTACAAATAGAA 1186
Qy 1659 TTTGAGCATCAGTGAGGTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAAC 1718
Db 1187 TTTGAGCATCAGTGAGGTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAAC 1246
Qy 1719 ATGTTCTCGGATCAGTGAGCTTTTATCTTTGTAAGACAAATTTGAGAGGCC 1778
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Qy 1779 TCACAGAGCCCTGCGCTCTGCTCAACTAGCAGATACAGGATGAGGCAGCCTGACCTC 1838
Db 1307 TCACAGAGCCCTGCGCTCTGCTCAACTAGCAGATACAGGATGAGGCAGCCTGACCTC 1366
Qy 1839 TTAAGAGGCTGAGAGCCCAACTGCTGCTCCCAACATGCATCTTCTTGAAGGTATG 1898
Db 1367 TTAAGAGGCTGAGAGCCCAACTGCTGCTCCCAACATGCATCTTCTTGAAGGTATG 1426
Qy 1899 GTACAGCAATGCTGCCCTTGGAGGAAAGAACTTAAGTAGATAGGAAATTAAGAAC 1958
Db 1427 GTACAGCAATGCTGCCCTTGGAGGAAAGAACTTAAGTAGATAGGAAATTAAGAAC 1486
Qy 1959 ACTATAATCTTCCACCTTAGGAATACTCCTGTTAATATAGGTGATCATCTTCCCTGAT 2018
Db 1487 ACTATAATCTTCCACCTTAGGAATACTCCTGTTAATATAGGTGATCATCTTCCCTGAT 1546
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Qy 2079 GTTAGAGTGCTTTAATGAATAAACATTTGTAGATCCTCTTTAATGGGTAACAGCA 2137
Db 1607 GTTAGAGTGCTTTAATGAATAAACATTTGTAGATCCTCTTTAATGGGTAACAGCA 1665

RESULT 10
HUMHCD8A HUMHCD8A 7319 bp DNA linear PRI 07-JAN-1995
LOCUS Human MHC class I CD8 alpha-chain (Leu-2/T8) gene, complete cds.
DEFINITION
ACCESSION M27161
VERSION M27161.1 GI:187844
KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 7319)
AUTHORS Nakayama,K., Tokito,S., Okumura,K. and Nakauchi,H.
TITLE Structure and expression of the gene encoding CD8 alpha chain
(Leu-2/T8)
JOURNAL Immunogenetics 30 (5), 393-397 (1989)
PUBMED 2509342
COMMENT Original source text: Human DNA, clone pLE2B13.5.
Draft entry and computer-readable sequence for [1] kindly submitted
by K.-i.Nakayama, 31-AUG-1989.
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source 1..7319
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/mol_type="genomic DNA"
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/map="2p12"
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238..256
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VLSNPTSGGSGWLFQPRGAASPTFLYLSONKPKAAEGLDTFQFSGKRLGDTFVLT
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2017..2127
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Best Local Similarity 98.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
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Db 5487 GCTTTCTCTCTTTCAGGCGCTGTGTCAAAATCGGGAGACAAGCCAGCGCTTTTCGGCGAGA 5546
Qy 819 TACGTCTAACCTGTGCAACGCCACTACATTTACTTCAAACTGAGATCCTTCTCTTTGAG 878
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Db 5607 GGAGCAAGTCCTTCCCTTTCATTTTTCAGTCTTCTCCCTCGTGTATTCATCTCATGA 5666
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Db 5667 TTATTATTTTAGTGGGGCGGGTGGGAAAGATTACTTTTCTTTATGTGTTGACGGGA 5726
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Db 5727 AACAAAACCTAGTAAAATCTACGTACACCAAGGGGTCACAATACTGTGTGCGCACAT 5786
Qy 1059 CGCGGTAGGCGTGGAAAGGGCGAGGCCAGAGCTACCCGAGAGTTCTCAGAAATCATGCT 1118
Db 5787 CGCGGTAGGCGTGGAAAGGGCGAGGCCAGAGCTACCCGAGAGTTCTCAGAAATCATGCT 5846
Qy 1119 GAGAGAGCTGGAGGCCACCCATGCCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGG 1178
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Db 5847 GAGAGAGCTGGAGGCCACCATGCAATCTCAACCTCTTCCCGCCCTTTTACAAAGGGG 5906
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Db 5907 AGGCTAAAGCCAGAGACAGCTTGATCAAGGACACACAGCACTAGGCTTGAGCAGTA 5966
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Db 6387 ATTGTAGCATCAGTGAAGTTAACTAAAGCCCTCTTGAATCTCTGAATTTGAGATCAA 6446
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QY 1898 GGTACAAGCAATGCTGCTGCCATTTGGAGAGAAAAAATCTTAAGTAGATAAGGAAATAAGAAC 1957
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Db 6747 TTATTTCTACACATACATGTAATATGCTCTTTCTTTTAAATAGGTTGCTACTATGC 6806
QY 2078 TGTATAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAACAGCA 2137
Db 6807 TGTATAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAACAGCA 6866

RESULT 11
G07115 LOCUS 1180 bp DNA linear STS 19-OCT-1995
DEFINITION human STS WI-9098, sequence tagged site.
ACCESSION G07115
VERSION G07115.1 GI:860360

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

STS: STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
Hudson.T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TCAGGTTGGAGCAGTAGCT
Primer B: TTGCCGTTGGAGACTCAAG
STS size: 125
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from M12824 -- Unigene.

FEATURES
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Location/Qualifiers
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/map="713_E_9; 774_F_9; 855_H_7; 842_A_10; 937_B_12;
(893-900)_C_12"
STS
primer_bind
395..519
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395..414
complement(501..519)
ORIGIN

Query Match 51.5%; Score 1164.2; DB 7; Length 1180;
Best Local Similarity 98.8%; Pred. No. 6.5e-299;
Matches 1166; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 828 CCTGTGCAACGACCACTACATTACTTCAAACTGAGATCCTTCTTTTGGAGGAGCAAGT 887
Db 1 CCTGTGCAACGACCACTACATTACTTCAAACTGAGATCCTTCTTTTGGAGGAGCAAGT 60
QY 888 CCTTCCCTTTTCAATTTTTCAGTCTTCTCCCTGATGATTCATTCTCATGATTATATTT 947
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Db 121 TAGTGGGGCGGGGGGAAAGATTACTTTTCTTTTATGTGTTTGCAGCGGAAACAAACT 180
QY 1008 AGGTAAATCTACAGTACACCAAGGGTCAATACTGTTGTGGGCACATCGCGGTAGG 1067

Db 181 AGGTAAATCTACAGTACACCAAGGTCACAATCTGTTGCGCACATCGCGGTAGG 240
Qy 1068 GCGTGGAAAGGGGAGGCGAGCTACCGCAGAGTCTCAGAAATCATGCTGAGAGAGCT 1127
Db 241 GCGTGGAAAGGGGAGGCGAGGCTACCGCAGAGTCTCAGAAATCATGCTGAGAGAGCT 300
Qy 1128 GGAGGCACCATGCCATCTCAACCTCTTCCCGCCCGTCTTCAAAAGGGGAGGCTAAAG 1187
Db 301 GGAGGCACCATGCCATCTCAACCTCTTCCCGCCCGTCTTCAAAAGGGGAGGCTAAAG 360
Qy 1188 CCCAGAGACAGCTTGATCAAAAGGCACAGCAAGTCAGGTTGGAGCAGTAGCTGGAGGG 1247
Db 361 CCCAGAGACAGCTTGATCAAAAGGCACAGCAAGTCAGGTTGGAGCAGTAGCTGGAGGG 420
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Db 1081 ATGCTGCTGCTTGGAG 1140
Qy 1968 TCTTCACCTTAGGAG 2007
Db 1141 TCTTCACCTTAGGAG 1180

RESULT 12
LOCUS CQ725925 1059 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 11859 from Patent WO2068579.
ACCESSION CQ725925

VERSION CQ725925.1 GI:42287423
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 11859 06-SEP-2002;
PE Corporation (NY) (US)
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source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 46.8%; Score 1059; DB 2; Length 1059;
Best Local Similarity 100.0%; Pred. No. 6.6e-271;
Matches 1059; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 CCTCACTGAGCGACTTCGCGCGAGAGAAAGAGGCTACTATTTCTGCTCGGCGCTGAG 420
Qy 476 CAATCTCATGCTACTTACGCTTCTGCGCGCTTCTCTGCGCGAGAGAGAGAGAGAGAGAG 535
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RESULT 13
AC169881/c
LOCUS
DEFINITION
Macaca mulatta clone CH250-110A2, *** SEQUENCING IN PROGRESS ***,
20 unordered pieces.
AC169881
VERSION
HTG; HTGS PHASE1.
KEYWORDS
SOURCE
Macaca mulatta (rhesus monkey)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 72869)
Muzny D.M., Abraham K.K., Abulimiti, A., Adams, C.Q., Aduba, G.,
Allen, C.C., Alsbrooks, S.L., Anosike, U.S., Archer, P.M.,
Arrondo, H.H., Attaway, T., Bandaranaike, D.P., Bangura, L.,
Barton, S.R., Bell, A.V., Bell, S.N., Beraducci, A.R., Bickham, C.,
Biswal, K., Blyth, P.R., Buhay, C.J., Canada, A., Cardenas, V.,
Carter, K., Chacko, J., Chandrasekhar, M.N., Chavez, D.,
Chen, G., Chen, R., Chu, H., Clerc, blankenburg, K.P., Cockrell, R.,
Cooper, J.A., Coyle, M.D., Cree, A., Cueto, C.B., Curry, S.M., Dai, W.,
Dao, M.D., Davila, M., Davis, C., Davy-Carroll, L., Del fierro, P.,
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Espinosa, V.C., Fa, M., Fernandez, S., Fernando, P.R., Ferrer, A.R.,
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Ganadharan, M., Ganer, J., Garcia, J., Garcia, J., Garcia, A.M.,
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Haynes, S.J., Hemphill, L., Hernandez, J., Hines, S., Hirani, K.,
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Howell, L.L., Hulyk, S.W., Hume, J., Jackson, A., Jackson, L.R.,
Jacob, S.K., Jiang, S.N., Jiang, H., Johnson, B., Johnson, R.,
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Keebler, J., Khan, Z.M., Kidwai, S., King, L.M., Kisamo, H., Kovar, C.L.,
Kovis, A.N., Kowis, C.R., Lago, L.A., Lago, M.T., Lai, C., Lara, P.,
Le, T.T., Lee, S.L., Lee, T.W., Legall, J., Lemmon, S.J.,
Lewis, L.R., Li, B., Li, Y., Li, Z., Linnell, M.A., Liu, J., Liu, W.,
Liu, Y., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensu, L.M.,
Lozano, R.J., Luc, T., Madu, R.C., Maheshwari, M., Maheshwari, R.,
Malloy, K., Mansouri, D.L., Martinez, E., Matejkova, P., Mathew, T.,
McCauley, S.K., McPherson, J.D., Mercado, C., Mercado, I.C.,
Metzker, M.B., Millin, A., Milosavljevic, A., Morgan, M.B., Morris, S.,
Munida, M., Murray, D.D., Muzny, D.M., Nazareth, L.V., Ngo, D.N.,
Nguyen, H.T., Nguyen, N.B., Nguyen, P.Q., Nwaokeme, O.O.,

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Obregon, M., Odeh, E.A., Okonkwo, F., Okwuonu, G.O., Okwuonu, K.C.,
Onyenekwe, J., Parish, B.J., Parker, D.N., Parra, A.A., Pasternak, S.,
Patel, B.M., Patel, R.R., Paul, H.A., Perez, A., Perez, L.M., Puzo, M.,
Perez, Y., Pham, T.L., Player, E.J., Primus, E.L., Pu, L., Puzo, M.,
Purkiss, C., Qin, X., Quiroz, J.B., Rabata, D., Rachlin, E.K., Ren, Y.,
Richards, S., Rojas, A., Ruiz, S., Sabo, A., Santibanez, J.,
Savory, G.G., Scherer, S.E., Schneider, B.W., Sebasigari, R.,
Sexton, M.M., Shen, H., Shen, Y., Sisson, I., Sneed, A.J., Sodergren, E.,
Song, X., Sorelle, R.P., Svatek, A.F., Taylor, E.W., Taylor, T.R.,
Thelus, R., Thomas, N., Thorn, R.D., Thornton, R.D., Tong, M.Y.,
Trejos, Z.Y., Umani, K., Vargo, C.E., Vattathil, S., Vega, R.A.,
Villasana, D., Volkov, A., Walker, D.L., Wang, Q., Wang, S.,
Willard, J.T., Watt, J.E., Wei, X., Wheeler, D.A., White, C.S., Williams
jr, R.L., Williams, A.C., Williams, G.A., Williams, J.D., Wilson, K.,
Woodworth, J.R., Worley, K.C., Wright, R.A., Wu, J., Wu, W., Yakub, S.,
Yerrapragada, S., Yu, F., Yuan, D.T., Yuan, Y., Zhang, J., Zhang, L.,
Zhang, Z., Zhou, J., Zhu, Y., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 72869)
Worley, K.C.
Direct Submission
Submitted (12-OCT-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
----- Project Information
Center project name: LBOOK
Center clone name: CH250-110A2
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 83719 bases at least Q40
Consensus quality: 87952 bases at least Q30
Consensus quality: 90578 bases at least Q20
Estimated insert size: 97635; sum-of-contrigs estimation
Quality coverage: 1x in Q20 bases; sum-of-contrigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 4285: contig of 2432 bp in length
* 6717: gap of unknown length
* 6817: contig of 2739 bp in length
* 9556: gap of unknown length
* 9656: contig of 2485 bp in length
* 12141: contig of 2485 bp in length
* 12240: gap of unknown length
* 14405: contig of 2165 bp in length
* 14505: gap of unknown length
* 14506: contig of 5162 bp in length
* 19668: gap of unknown length
* 19767: contig of 3536 bp in length
* 23303: contig of 3536 bp in length
* 23404: gap of unknown length
* 25996: contig of 2593 bp in length
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* 28973: gap of unknown length
* 35138: contig of 6066 bp in length
* 35139: gap of unknown length

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

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* 56841 56940: gap of unknown length
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* 59703 59802: gap of unknown length
* 59803 63695: contig of 3893 bp in length
* 63696 63795: gap of unknown length
* 63796 68927: contig of 5132 bp in length
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FEATURES

source

Location/Qualifiers

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Matches 1266; Conservative 0; Mismatches 110; Indels 107; Gaps 4;

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| ORGANISM | | | |
| Unknown. | | | |
| REFERENCES | | | |
| 1 (bases 1 to 1060) | | | |
| Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A. | | | |
| Soluble and its use in B cell stimulation | | | |
| Patent: US 5540926-A 11 30-JUL-1996; | | | |
| JOURNAL | | | |
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| Qy | 367 | GGCTGGACACCCAGCGGTTCTCGGCGAAGAGTTGGGGGACACCTTCTCTCACCCCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTTCTCGGCGAAGAGTTGGGGGACACCTTCTCTCACCCCTGA | 372 |
| Qy | 427 | GCAGCTTCCGCGGAGAAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACTCCATCA | 486 |

Search completed: May 30, 2006, 09:01:49
Job time : 12409 secs

| | | | |
|----|------|--|------|
| Qy | 67 | CGCTCCCTCGCCCGAGCTTCGAGCAAGCAGCGTCTGGGAGCGGCTCATGSCCT | 126 |
| Db | 13 | CGCTCCCTCGCCCGAGCTTCGAGCAAGCAGCGTCTGGGAGCGGCTCATGSCCT | 72 |
| Qy | 127 | TACAGTGACCGCTTGTCTCGCTCGCTGGGCTTGTCTCCAGCGCCAGGCGGAGCC | 186 |
| Db | 73 | TACAGTGACCGCTTGTCTCGCTCGCTGGGCTTGTCTCCAGCGCCAGGCGGAGCC | 132 |
| Qy | 187 | AGTTCCGGGTGTCCGCTCGATCGGACCTGGGCGAGACAGTGGAGCTGAAGT | 246 |
| Db | 133 | AGTTCCGGGTGTCCGCTCGATCGGACCTGGGCGAGACAGTGGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGGTGCTGTCTGTCACACCGAGCGTGGGCTGTCTGTGGCTCTTCAGCGCGCGGCG | 306 |
| Db | 193 | GCCAGGTGCTGTCTGTCACACCGAGCGTGGGCTGTCTGTGGCTCTTCAGCGCGCGGCG | 252 |
| Qy | 307 | CCGCGCCAGTCCACACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCGCGGAGG | 366 |
| Db | 253 | CCGCGCCAGTCCACACCTTCTCTATACCTCTCCCAAAACAAGGCGCGCGGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCACCTTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCACCTTGA | 372 |
| Qy | 427 | GCGATTCCGCGGAGAGAAAGAGGCTACTATTTCTGCTCGGCTGTGAGCAACTCCATCA | 486 |
| Db | 373 | GCGATTCCGCGGAGAGAAAGAGGCTACTATTTCTGCTCGGCTGTGAGCAACTCCATCA | 432 |
| Qy | 487 | TGTACTTCAGCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACACGAGCGGCGGCG | 546 |
| Db | 433 | TGTACTTCAGCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACACGAGCGGCGGCG | 492 |
| Qy | 547 | CGGACACCAACACCGCGGCCACCATCGCGTCCGAGCCCTGTCTCCGCGCCAGAGG | 606 |
| Db | 493 | CGGACACCAACACCGCGGCCACCATCGCGTCCGAGCCCTGTCTCCGCGCCAGAGG | 552 |
| Qy | 607 | CGTGCGGCCAGCGCGCGGGCGGAGTGCAACAAGAGGGGCTGGACTTCGCCCTGTGATA | 666 |
| Db | 553 | CGTGCGGCCAGCGCGCGGGCGGAGTGCAACAAGAGGGGCTGGACTTCGCCCTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGGCGCCCTTGGCGGGACTGTGGGCTCTCTCTGTCACCTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGGCGCCCTTGGCGGGACTGTGGGCTCTCTCTGTCACCTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACCAAGAGAACCGAGACGTGTTTGCAAAATGTCCCGGCTGTGTCA | 786 |
| Db | 673 | CCCTTTACTGCAACCAAGAGAACCGAGACGTGTTTGCAAAATGTCCCGGCTGTGTCA | 732 |
| Qy | 787 | AATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAACCTGTGTGCAACAGCCACTA | 846 |
| Db | 733 | AATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAACCTGTGTGCAACAGCCACTA | 792 |
| Qy | 847 | CATTACTTCAAACTGAGATCTTCTTTGAGGGAGCAAGTCTTCCCTTTTCATTTTTTC | 906 |
| Db | 793 | CATTACTTCAAACTGAGATCTTCTTTGAGGGAGCAAGTCTTCCCTTTTCATTTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCTGTGTATTCATTCATGATTAATTTTAGTGGGGGGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCTGTGTATTCATTCATGATTAATTTTAGTGGGGGGGGTGGGA | 912 |
| Qy | 967 | AAGATTACTTTTCTTTATGTGTTGACGGGAAACAAAAGTAGGTAAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTACTTTTCTTTATGTGTTGACGGGAAACAAAAGTAGGTAAATCTACAGTACA | 972 |
| Qy | 1027 | CCACAAGGTCACATACCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC | 1086 |
| Db | 973 | CCACAAGGTCACATACCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC | 1032 |
| Qy | 1087 | AGAGCTACCCGAGAGTTCTCAGAATCA | 1114 |
| Db | 1033 | AGAGCTACCCGAGAGTTCTCAGAATCA | 1060 |

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 29, 2006, 21:45:26 ; Search time 2523 Seconds
(without alignments)
6248.218 Million cell updates/sec
Title: US-10-804-763-2
Perfect score: 2261
Sequence: 1 gaatcaggctccggccgg.....aaaaaaaaaaaaaaaaaaaa 2261
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 2261 | 100.0 | 2261 | 12 | ADP10406 Reference |
| 2 | 2261 | 100.0 | 2261 | 13 | ADG92791 Nucleotid |
| 3 | 2261 | 100.0 | 2261 | 13 | ADG19437 DNA of th |
| 4 | 2261 | 100.0 | 2261 | 14 | ADW86779 Human CD8 |
| 5 | 2261 | 100.0 | 2261 | 14 | ADZ26401 Human CD8 |
| 6 | 2132.8 | 94.3 | 3048 | 12 | ADQ64633 Novel hum |
| 7 | 2061.6 | 91.2 | 2134 | 12 | ADQ22926 Human sof |
| 8 | 2061.2 | 91.2 | 2123 | 10 | ADP90782 Human hep |
| 9 | 2029 | 89.7 | 2150 | 13 | ADG92793 cDNA of a |
| 10 | 2029 | 89.7 | 2150 | 13 | ADG19439 Human sec |
| 11 | 2029 | 89.7 | 2150 | 14 | ADZ26403 Human CD8 |
| 12 | 1905 | 84.3 | 3518 | 14 | AED96282 Human C-r |
| 13 | 1821 | 80.5 | 3476 | 14 | AED96284 Human C-r |
| 14 | 1683 | 74.4 | 3407 | 14 | AED96285 Human C-r |
| 15 | 1683 | 74.4 | 3743 | 14 | AED96281 Human C-r |
| 16 | 1393 | 61.6 | 4392 | 14 | AED96283 Human C-r |
| 17 | 1361.4 | 60.2 | 1729 | 12 | ADQ18424 Human sof |
| 18 | 1361.4 | 60.2 | 1729 | 13 | ACF87521 Human SIR |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | | |
|----|-------|------|------|----|----------|-----------------|
| 19 | 1048 | 46.4 | 1060 | 2 | AAQ57986 | Genomic s |
| 20 | 1048 | 46.4 | 1060 | 10 | ADD25612 | Binding d |
| 21 | 1048 | 46.4 | 1060 | 11 | ADI31688 | Human CDN |
| 22 | 1048 | 46.4 | 1060 | 13 | ADS83755 | Human lym |
| 23 | 761.4 | 33.7 | 773 | 3 | AAZ29002 | Human CD8 |
| 24 | 744 | 32.9 | 744 | 14 | AED96294 | Human C-r |
| 25 | 708 | 31.3 | 708 | 2 | AAZ80967 | Human CD8 |
| 26 | 708 | 31.3 | 708 | 8 | ABZ69260 | Human CD8 |
| 27 | 708 | 31.3 | 708 | 13 | ADS92817 | Nucleotid |
| 28 | 708 | 31.3 | 708 | 13 | ADS19462 | Coding se |
| 29 | 708 | 31.3 | 708 | 14 | ADV42461 | Human psy |
| 30 | 708 | 31.3 | 708 | 15 | AEF68357 | Human CD8 |
| 31 | 704.8 | 31.2 | 708 | 8 | ABZ69262 | Human CD8 |
| 32 | 676 | 29.9 | 727 | 10 | ADF90668 | Human hep |
| 33 | 646.4 | 28.6 | 662 | 12 | ADN11772 | Human CD8 |
| 34 | 644.4 | 28.5 | 1637 | 12 | ADN11778 | Human CD8-5A/B- |
| 35 | 644.4 | 28.5 | 2909 | 12 | ADN11779 | CD8-NS2/3 |
| 36 | 610.4 | 27.0 | 708 | 13 | ADS92815 | Nucleotid |
| 37 | 610.4 | 27.0 | 708 | 13 | ADS19461 | DNA of th |
| 38 | 610 | 27.0 | 610 | 12 | ADO41257 | Human CDN |
| 39 | 593 | 26.2 | 610 | 13 | ADU12274 | Solid tum |
| 40 | 586 | 25.9 | 599 | 12 | ADO41256 | Human CDN |
| 41 | 557.4 | 24.7 | 2001 | 13 | ADS92807 | Nucleotid |
| 42 | 557.4 | 24.7 | 2001 | 13 | ADS19453 | DNA of th |
| 43 | 552 | 24.4 | 1891 | 13 | ADS92809 | Nucleotid |
| 44 | 552 | 24.4 | 1891 | 13 | ADS19455 | DNA of th |
| 45 | 543 | 24.0 | 1131 | 3 | AAZ46253 | CDNA enco |

ALIGNMENTS

RESULT 1
ADP10406
ID ADP10406 standard; DNA; 2261 BP.
XX
AC ADP10406;
XX

DT 12-AUG-2004 (first entry)
XX

DE Reference mRNA sequences for marker probe #83.
XX

KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX

OS Homo sapiens.
XX

PN WO2004042346-A2.
XX

PD 21-MAY-2004.
XX

PF 24-APR-2003; 2003WO-US012946.
XX

PR 24-APR-2002; 2002US-00131831.
XX

PR 20-DEC-2002; 2002US-00325899.
XX

(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX

Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX

WPI; 2004-400724/37.
XX

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
the genes.
XX

PS Claim 80; SEQ ID NO 415; 1762bp; English.
XX

CC The present invention relates to diagnosing or monitoring transplant
rejection, e.g. cardiac or kidney transplant rejection, in an individual
comprises detecting the expression level of one or more genes. The

from plasmid only
seq
note

CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.
XX
SQ

Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 12; Length 2261;

Best Local Similarity 100.0%; Pred. No. 1.8e-308;

Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | GAATCAGGCTCCGGGCGCGGCGGAAGGGCGCAACTTCCCGCTCGGCGGCCACCGGCT | 60 |
| Db | 1 | GAATCAGGCTCCGGGCGCGGCGGAAGGGCGCAACTTCCCGCTCGGCGGCCACCGGCT | 60 |
| Qy | 61 | CCGCGGCGCTCCCTCGCGCGCGAGCTTCGAGCCAGCAGCTCTCGGGAGCGCGTCA | 120 |
| Db | 61 | CCGCGGCGCTCCCTCGCGCGCGAGCTTCGAGCCAGCAGCTCTCGGGAGCGCGTCA | 120 |
| Qy | 121 | TGGCCTTACCAAGTACCGCTTGCTTCCTGCGCTGGCTTGCTGCCACCGCGCAGGC | 180 |
| Db | 121 | TGGCCTTACCAAGTACCGCTTGCTTCCTGCGCTGGCTTGCTGCCACCGCGCAGGC | 180 |
| Qy | 181 | CGAGCCAGTTCGGGTGTGCGGCTGGATCGAACCTGGAACTGGGGCAGACAGTGGAGC | 240 |
| Db | 181 | CGAGCCAGTTCGGGTGTGCGGCTGGATCGAACCTGGAACTGGGGCAGACAGTGGAGC | 240 |
| Qy | 241 | TGAAGTCCAGGTGCTGTCTCAACCGAGTGGGGTGTCTGGGTCTTCAGACCGC | 300 |
| Db | 241 | TGAAGTCCAGGTGCTGTCTCAACCGAGTGGGGTGTCTGGGTCTTCAGACCGC | 300 |
| Qy | 301 | CGCGCGCGCGCCAGTCCACCTTCCTCTATACCTCTCCCAAAAGCCCAAGGCGG | 360 |
| Db | 301 | CGCGCGCGCGCCAGTCCACCTTCCTCTATACCTCTCCCAAAAGCCCAAGGCGG | 360 |
| Qy | 361 | CGAGGGGCTGACACACAGCGGTCTCGGGCAGAGGTGGGGACACCTTCGCTCA | 420 |
| Db | 361 | CGAGGGGCTGACACACAGCGGTCTCGGGCAGAGGTGGGGACACCTTCGCTCA | 420 |
| Qy | 421 | CCCTGAGCGACTTCGCGCAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCAACT | 480 |
| Db | 421 | CCCTGAGCGACTTCGCGCAGAGAACGAGGCTACTATTCTGCTCGGCCCTGAGCAACT | 480 |
| Qy | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCCAGCGAAGCCACACGACGC | 540 |
| Db | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCCAGCGAAGCCACACGACGC | 540 |
| Qy | 541 | CAGCGCGCGACCAACACACCGCGGCCACCATCGGTGCGAGCCCTGCTCGGCC | 600 |
| Db | 541 | CAGCGCGCGACCAACACACCGCGGCCACCATCGGTGCGAGCCCTGCTCGGCC | 600 |
| Qy | 601 | CAGGGCGTCCGCGCAGCGCGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCT | 660 |
| Db | 601 | CAGGGCGTCCGCGCAGCGCGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCT | 660 |
| Qy | 661 | GTGATATCTACTCTGGCGGCTTCGGCGGGACTTGTGGGTCTCTCTCTGTCACTGG | 720 |
| Db | 661 | GTGATATCTACTCTGGCGGCTTCGGCGGGACTTGTGGGTCTCTCTCTGTCACTGG | 720 |
| Qy | 721 | TTATCACCCCTTACTTGCAACACACAGAACCGAGACGTGTTTGCAAAATGTCGGGCTG | 780 |
| Db | 721 | TTATCACCCCTTACTTGCAACACACAGAACCGAGACGTGTTTGCAAAATGTCGGGCTG | 780 |
| Qy | 781 | TGGTCAAAATCGGGAGACAGCCAGCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 840 |
| Db | 781 | TGGTCAAAATCGGGAGACAGCCAGCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 840 |

| | | | |
|----|------|--|------|
| Qy | 841 | CCACTACATTACTTCAAACTGAGATCCTTCTCTTTTGGGGAGCAAGTCCCTTCCCTTTCAT | 900 |
| Db | 841 | CCACTACATTACTTCAAACTGAGATCCTTCTCTTTTGGGGAGCAAGTCCCTTCCCTTTCAT | 900 |
| Qy | 901 | TTTTTCCAGCTTCCCTCCCTGTGATTCATCTCATGATTATTATTTAGTGGGGCGGG | 960 |
| Db | 901 | TTTTTCCAGCTTCCCTCCCTGTGATTCATCTCATGATTATTATTTAGTGGGGCGGG | 960 |
| Qy | 961 | GTGGGAAAGATTACTTTTTTCTTTATGTGTTTGAACGGGAAACAAAACCTAGGTAAATCTAC | 1020 |
| Db | 961 | GTGGGAAAGATTACTTTTTTCTTTATGTGTTTGAACGGGAAACAAAACCTAGGTAAATCTAC | 1020 |
| Qy | 1021 | AGTACACCAAGGGTCAAAATATCTGTTGTGCGGCATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Db | 1021 | AGTACACCAAGGGTCAAAATATCTGTTGTGCGGCATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Qy | 1081 | CAGCCAGAGTACCCCGCAGAGTTCAGAAATCATGCTGAGAGAGCTGGAGCACCCATG | 1140 |
| Db | 1081 | CAGCCAGAGTACCCCGCAGAGTTCAGAAATCATGCTGAGAGAGCTGGAGCACCCATG | 1140 |
| Qy | 1141 | CCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT | 1200 |
| Db | 1141 | CCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT | 1200 |
| Qy | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGGACCTTGTCTCCA | 1260 |
| Db | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGGACCTTGTCTCCA | 1260 |
| Qy | 1261 | GCTCAGGGCTTTCCTCCACACCATTCAGCTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Db | 1261 | GCTCAGGGCTTTCCTCCACACCATTCAGCTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Qy | 1321 | TGAGGTGCTTGAGTCTCCACGCAAGGAAACAAGTACTTCTTGATACCTGGGATACTGT | 1380 |
| Db | 1321 | TGAGGTGCTTGAGTCTCCACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATACTGT | 1380 |
| Qy | 1381 | GCCCAGAGCTTCGAGGAGGTAATGAAATTAAGAGAGAACTGCCTTTGGCAGAGTCTAT | 1440 |
| Db | 1381 | GCCCAGAGCTTCGAGGAGGTAATGAAATTAAGAGAGAACTGCCTTTGGCAGAGTCTAT | 1440 |
| Qy | 1441 | AATGTAAACATATCAGACTTTTTTTTTTATATACTCAAGCCTAAATTTGATAGACCTAA | 1500 |
| Db | 1441 | AATGTAAACATATCAGACTTTTTTTTTTATATACTCAAGCCTAAATTTGATAGACCTAA | 1500 |
| Qy | 1501 | AATAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 |
| Db | 1501 | AATAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 |
| Qy | 1561 | CTCTGTGAACCCCTATGTGGAGGGGAATGCTCTCCAGCCCTTGATTCGAGAGGG | 1620 |
| Db | 1561 | CTCTGTGAACCCCTATGTGGAGGGGAATGCTCTCCAGCCCTTGATTCGAGAGGG | 1620 |
| Qy | 1621 | CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTAAA | 1680 |
| Db | 1621 | CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTAAA | 1680 |
| Qy | 1681 | CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAATGCTTCCTGGGATCACTGATGA | 1740 |
| Db | 1681 | CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAATGCTTCCTGGGATCACTGATGA | 1740 |
| Qy | 1741 | CTTTTATATCTTTGTAAAGACAAATTTGGAGAGCCCTTCACACAGCCCTGGCCCTGTGT | 1800 |
| Db | 1741 | CTTTTATATCTTTGTAAAGACAAATTTGGAGAGCCCTTCACACAGCCCTGGCCCTGTGT | 1800 |
| Qy | 1801 | CAACTAGCAGATACAGGGATGAGCAGACCTGACTCTCTTAAGAGGCTGAGAGGCCAAA | 1860 |
| Db | 1801 | CAACTAGCAGATACAGGGATGAGGAGACCTGACTCTCTTAAGAGGCTGAGAGGCCAAA | 1860 |
| Qy | 1861 | CTGCTGTCCCAACATGCACTTCTCTTGTCTTAAGGTATGGTACAGCAATGCTGCCCATTT | 1920 |
| Db | 1861 | CTGCTGTCCCAACATGCACTTCTCTTGTCTTAAGGTATGGTACAGCAATGCTGCCCATTT | 1920 |

| | | | |
|----|------|--|------|
| Qy | 901 | TTTTCCAGCTTCTCCTCGTGTATTCATCTCATGATTATTTTAGTGGGGGGG | 960 |
| Ds | 901 | TTTTCCAGCTTCTCCTCGTGTATTCATCTCATGATTATTTTAGTGGGGGGG | 960 |
| Qy | 961 | GTGGAAAGATTACTTTTTCTTTATGCTTTTGACGGGAAACAAACTAGGTAAATCTAC | 1020 |
| Ds | 961 | GTGGAAAGATTACTTTTTCTTTATGCTTTTGACGGGAAACAAACTAGGTAAATCTAC | 1020 |
| Qy | 1021 | AGTACACCAAGGGTCACAATCTGTTGTGCGCACATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Ds | 1021 | AGTACACCAAGGGTCACAATCTGTTGTGCGCACATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Qy | 1081 | CAGGCAGAGCTACCCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCCACCCATG | 1140 |
| Ds | 1081 | CAGGCAGAGCTACCCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCCACCCATG | 1140 |
| Qy | 1141 | CCATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT | 1200 |
| Ds | 1141 | CCATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT | 1200 |
| Qy | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| Ds | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| Qy | 1261 | GCTCAGGCTCTTTCTCCACACCATTCAGGTCCTTTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Ds | 1261 | GCTCAGGCTCTTTCTCCACACCATTCAGGTCCTTTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Qy | 1321 | TGAGTGTCTGAGTCTCAAGCGCAAGGAACTGCTTTTGGAGGAGGTTCTAT | 1380 |
| Ds | 1321 | TGAGTGTCTGAGTCTCAAGCGCAAGGAACTGCTTTTGGAGGAGGTTCTAT | 1380 |
| Qy | 1381 | GCCAGAGCTCGAGGAGTAAATGAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT | 1440 |
| Ds | 1381 | GCCAGAGCTCGAGGAGTAAATGAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT | 1440 |
| Qy | 1441 | AATGTAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAATGTATAGACCTAA | 1500 |
| Ds | 1441 | AATGTAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAATGTATAGACCTAA | 1500 |
| Qy | 1501 | AATAAATGAAGTGTGAGCTTAAACCTGGGAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 |
| Ds | 1501 | AATAAATGAAGTGTGAGCTTAAACCTGGGAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 |
| Qy | 1561 | CTCTGTGAAACCCCTATGTGGAGGCGAATGCTCTCCAGCCCTTGCAATGCAGAGGG | 1620 |
| Ds | 1561 | CTCTGTGAAACCCCTATGTGGAGGCGAATGCTCTCCAGCCCTTGCAATGCAGAGGG | 1620 |
| Qy | 1621 | CCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAA | 1680 |
| Ds | 1621 | CCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAA | 1680 |
| Qy | 1681 | CTAAGGCCCTCTTGAATCTCTGAAATTCAGATACAAACATGTTCTGGGATCAGTGATGA | 1740 |
| Ds | 1681 | CTAAGGCCCTCTTGAATCTCTGAAATTCAGATACAAACATGTTCTGGGATCAGTGATGA | 1740 |
| Qy | 1741 | CTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTTCAACAGCCCTGGCCCTCTGT | 1800 |
| Ds | 1741 | CTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTTCAACAGCCCTGGCCCTCTGT | 1800 |
| Qy | 1801 | CAATGAGAGATACAGGATAGGAGACCTGACTCTCTTAAGAGGCTGAGAGGCCAAA | 1860 |
| Ds | 1801 | CAATGAGAGATACAGGATAGGAGACCTGACTCTCTTAAGAGGCTGAGAGGCCAAA | 1860 |
| Qy | 1861 | CTGCTGCCCAACATGACTTCTTCTGCTTAGGTATGTACAAAGCAATGCTGCCCAT | 1920 |
| Ds | 1861 | CTGCTGCCCAACATGACTTCTTCTGCTTAGGTATGTACAAAGCAATGCTGCCCAT | 1920 |
| Qy | 1921 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAGAACCACTCATTAATTTCCACCTTAGG | 1980 |
| Ds | 1921 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAGAACCACTCATTAATTTCCACCTTAGG | 1980 |

| | | | |
|----|------|--|------|
| Qy | 1981 | AATAATCTCTCTGTTAATATGCTGTACATCTTCTCTGATTATTTTCTACACATACATGTA | 2040 |
| Ds | 1981 | AATAATCTCTCTGTTAATATGCTGTACATCTTCTCTGATTATTTTCTACACATACATGTA | 2040 |
| Qy | 2041 | AATATGCTCTTCTTTTAAATAGGTTGTACTATGCTGTTTATGAGTGGCTTTAATGAAT | 2100 |
| Ds | 2041 | AATATGCTCTTCTTTTAAATAGGTTGTACTATGCTGTTTATGAGTGGCTTTAATGAAT | 2100 |
| Qy | 2101 | AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAAAAAGAAAAAAGAAAAA | 2160 |
| Ds | 2101 | AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAAAAAGAAAAAAGAAAAA | 2160 |
| Qy | 2161 | AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 2220 |
| Ds | 2161 | AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 2220 |
| Qy | 2221 | AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 2281 |
| Ds | 2221 | AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 2281 |

RESULTS

ADSI9437

ID ADS19437 standard; DNA; 2261 BP.

XX ADS19437;

AC ADS19437;

XX 16-DEC-2004 (first entry)

XX DNA of the human CD8 alpha chain mRNA.

DE gene; ds; gene therapy; CD8 alpha chain; cellular immune response;

XX humoral immune response; immunosuppressive.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 120..827

XX /*tag= a

XX /product= "CD8 alpha chain protein"

XX WO2004083404-A2.

XX 30-SEP-2004.

XX 19-MAR-2004; 2004WO-US008567.

XX 19-MAR-2003; 2003US-0456378P.

XX (ISOG-) ISOGENIS INC.

XX Qi Y, Zhang X, Konigsberg PJ;

XX WPI; 2004-691049/67.

XX P-PSDB; ADS19436.

XX New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain operably linked to a nucleic acid encoding a transmembrane polypeptide, useful for inhibiting cellular and humoral components of the host immune responses.

XX Disclosure; Fig 1; 94pp; English.

XX This invention relates to novel gene therapy vectors with reduced immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8 alpha chain operably linked to nucleic acid encoding a transmembrane polypeptide and a second nucleic acid representing the therapeutic gene of interest (for example ornithine carbamoyl transferase or beta glucosidase), whereby transcriptional and translational control elements direct expression thereof. The present invention describes a method to reduce an immune response against antigens derived from a gene therapy delivery system i.e. improving the expression of a therapeutic transgene in a host and improving viral expression vectors with reduced

CC immunogenicity. Accordingly, these compositions are useful for inhibiting
CC both the cellular and humoral components of the host immune responses
CC against expression vectors and target cells transfected with the vectors.
CC As such, they exhibit immunosuppressive activity. This polynucleotide is
CC the DNA sequence of the human CD8 alpha chain mRNA of the invention.

```
Query Match      100.0%; Score 2261; DB 13; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|-----|-----|-----|---|-----|---|---|----|----|
| Qy | 1 | GA | A | N | A | T | C | A | G | G | T | C | C | C | T | C | G | G | C | G | C | G | C | G | A | A | G | G | G | C | A | C | T | T | C | C | C | C | C | T | C | G | G | C | C | C | C | C | A | C | C | G | G | T | C | | 60 |
| Db | 1 | GA | A | A | T | C | A | G | G | T | C | C | G | G | C | G | C | G | C | G | C | G | C | G | A | A | G | G | G | C | A | C | T | T | C | C | C | C | C | T | C | G | G | C | C | C | C | A | C | C | G | G | T | C | | 60 | |
| Qy | 61 | C | C | C | G | C | G | C | C | T | C | C | T | C | G | C | G | C | C | G | C | C | G | C | A | A | G | C | C | A | G | C | A | G | C | T | T | C | G | C | G | C | C | C | C | A | C | C | G | T | C | | 120 | | | | |
| Db | 61 | C | C | C | G | G | C | C | T | C | C | T | C | G | C | G | C | C | G | A | G | C | T | T | C | G | A | C | C | A | G | C | A | G | C | G | T | C | T | C | G | G | A | G | C | G | T | C | | 120 | | | | | | | |
| Qy | 121 | T | G | G | C | T | T | A | C | A | G | T | G | A | C | C | G | C | T | T | G | C | T | C | T | C | G | C | G | C | T | T | G | C | C | T | T | G | C | C | T | T | G | C | C | T | T | C | | 180 | | | | | | | |
| Db | 121 | T | G | G | C | T | T | A | C | A | G | T | G | A | C | C | G | C | T | T | G | C | T | C | T | C | G | C | G | C | T | T | G | C | C | T | T | G | C | C | T | T | G | C | C | T | | 180 | | | | | | | | | |
| Qy | 181 | C | G | A | C | C | A | G | T | T | C | C | G | G | T | G | T | G | A | T | C | G | A | C | T | T | G | A | A | C | T | T | G | A | A | C | T | T | G | A | A | C | T | T | G | A | A | C | | 240 | | | | | | | |
| Db | 181 | C | G | A | C | C | A | G | T | T | C | C | G | G | T | G | T | G | A | T | C | G | A | C | T | T | G | A | A | C | T | T | G | A | A | C | T | T | G | A | A | C | T | T | G | A | A | C | | 240 | | | | | | | |
| Qy | 241 | T | G | A | A | T | G | C | A | G | T | G | T | C | T | C | A | A | C | C | G | A | G | T | C | T | C | G | G | G | T | C | T | C | T | C | T | C | T | C | T | C | T | C | T | C | A | C | C | | 300 | | | | | | |
| Db | 241 | T | G | A | A | T | G | C | A | G | T | G | T | C | T | C | A | A | C | C | G | A | G | T | C | T | C | G | G | G | T | C | T | C | T | C | T | C | T | C | T | C | T | C | T | C | A | C | C | | 300 | | | | | | |
| Qy | 301 | G | C | G | C | G | C | G | C | C | A | G | T | C | C | C | A | C | T | T | C | T | C | T | A | T | A | C | T | C | T | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | A | | 360 | | | | | | | |
| Db | 301 | G | C | G | C | G | C | G | C | C | A | G | T | C | C | C | A | C | T | T | C | T | C | T | A | T | A | C | T | C | T | C | C | A | A | A | A | A | A | A | A | A | A | A | A | A | A | | 360 | | | | | | | | |
| Qy | 361 | C | C | G | A | G | G | G | C | T | G | A | C | A | C | C | A | G | T | T | C | T | C | G | G | A | A | G | A | G | T | T | G | G | G | A | C | A | C | T | T | C | G | T | C | A | | 420 | | | | | | | | | |
| Db | 361 | C | C | G | A | G | G | C | T | G | A | C | A | C | C | A | G | T | T | C | T | C | G | G | A | A | G | A | G | T | T | G | G | G | A | C | A | C | T | T | C | G | T | C | A | | 420 | | | | | | | | | | |
| Qy | 421 | C | C | T | G | A | G | C | A | C | T | T | C | C | G | C | G | A | G | A | C | A | G | G | G | T | A | C | T | A | T | T | T | C | T | C | T | C | T | C | T | C | T | C | T | C | A | | 480 | | | | | | | | |
| Db | 421 | C | C | T | G | A | G | C | A | C | T | T | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1981 AATAATCTCCGTTAAATAGTGTTACATTTCTCTCGATTATTTTCTACATACATGTAA 2040
Qy ADW86779
Db 2041 AATATGCTCTTTCTTTTAAATAGGTTGTACTATGCTGTATGAGTGCGCTTTAATGAAT 2100
Qy 2041 AATATGCTCTTTCTTTTAAATAGGTTGTACTATGCTGTATGAGTGCGCTTTAATGAAT 2100
Qy 2101 AAACATTTGTAGCATCTCTCTTTAATGGTTAAACAGCAAAAAAATTTTTTTTTTTTTTTT 2160
Db 2101 AAACATTTGTAGCATCTCTCTTTAATGGTTAAACAGCAAAAAAATTTTTTTTTTTTTTTT 2160
Qy 2161 AAAAAAATTT 2220
Db 2161 AAAAAAATTT 2220
Qy 2221 AAAAAAATTT 2261
Db 2221 AAAAAAATTT 2261

RESULT 4
ID ADW86779 standard; DNA; 2261 BP.
XX AC ADW86779;
XX DT 07-APR-2005 (first entry)
XX DE Human CD8 gene.
XX KW protein interaction; fusion protein; ss; PCR; primer.
XX OS Homo sapiens.
XX PN WO2005007822-A2.
XX PD 27-JAN-2005.
XX PF 09-JUL-2004; 2004WO-US021887.
XX PR 09-JUL-2003; 2003US-0485968P.
XX PR 15-OCT-2003; 2003US-0511918P.
XX PR 27-APR-2004; 2004US-0566113P.
XX (SENT-) SENTIGEN BIOSCIENCES INC.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Lee KJ, Axel R, Strapps W, Barnea G;
XX WPT; 2005-102091/11.
XX DR

Determining protein/protein interaction modulator comprises contacting the compound to a cell transformed or transfected with G-protein coupled receptor and arrestin.
XX Example 29; SEQ ID NO 99; 133pp; English.
XX The invention relates to a novel method for determining if a test-compound modulates a specific protein/protein interaction or protein interactions of interest. The method comprises contacting the compound to a cell or samples of cells, each of which has been transformed or transfected with a nucleic acid molecule. The invention further comprises: a recombinant cell, transformed or transfected with any of the nucleic acid molecules; an isolated nucleic acid molecule comprising, in 5' to 3' order, any of the nucleotide sequences described; an expression vector comprising the isolated nucleic acid molecule of above, operably linked to a promoter; a fusion protein produced by expression of the isolated nucleic acid molecule of above; and a test kit, useful for determining if a test compound modulates a specific protein/protein interaction of interest. The methods, nucleic acid molecules, and kit are useful for determining if a test-compound modulates a specific protein/protein interaction or protein interactions of interest. This polynucleotide sequence represents the human CD8 gene used in the method of the invention.

XX SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;
Query Match 100.0%; Score 2261; DB 14; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATCAGGCTCCGGGCGGGCGGAGGCGCAACTTTTCCCCCTCGGGCGCCACCAGGCT 60
Db 1 GAATCAGGCTCCGGGCGGGCGGAGGCGCAACTTTTCCCCCTCGGGCGCCACCAGGCT 60
Qy 61 CCGCGCGCTCTCCCTCGCGCCGAGCTTCAGCAACAGCAGCGCTCTGGGAGCGCGTCA 120
Db 61 CCGCGCGCTCTCCCTCGCGCCGAGCTTCAGCAACAGCAGCGCTCTGGGAGCGCGTCA 120
Qy 121 TGGCCTTACCAAGTGACCGCTTGTCTCTCGCGCTGGCTTGTCTGTCCACCGCCAGGC 180
Db 121 TGGCCTTACCAAGTGACCGCTTGTCTCTCGCGCTGGCTTGTCTGTCCACCGCCAGGC 180
Qy 181 CGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGGCGAGACAGTGGAGC 240
Qy 241 TGAAGTCCAGGTGCTGTCTGTCACACCGAGCTCGGGCTGTCTGTGGCTCTTCCAGCGCG 300
Db 241 TGAAGTCCAGGTGCTGTCTGTCACACCGAGCTCGGGCTGTCTGTGGCTCTTCCAGCGCG 300
Qy 301 GCGGCGCGCGCGCCAGTCCCACTTCTCTATATCTCTCCCAAAACAGCCCAAGGCGG 360
Db 301 GCGGCGCGCGCGCCAGTCCCACTTCTCTATATCTCTCCCAAAACAGCCCAAGGCGG 360
Qy 361 CCGAGGGGCTGGACACCGAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
Db 361 CCGAGGGGCTGGACACCGAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
Qy 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGTCTCGGCCCTTGAGCAACT 480
Db 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGTCTCGGCCCTTGAGCAACT 480
Qy 481 CCATCATGTACTTCCAGCCACTTCTGTGCGGCTCTTCTGCGAGGAGCCCAACGAGCGC 540
Db 481 CCATCATGTACTTCCAGCCACTTCTGTGCGGCTCTTCTGCGAGGAGCCCAACGAGCGC 540
Qy 541 CAGCGCGCGAGCACCAACACCGCGGCCACCATGCGCTCGAGCCCTGTCTCTCGGCC 600
Db 541 CAGCGCGCGAGCACCAACACCGCGGCCACCATGCGCTCGAGCCCTGTCTCTCGGCC 600
Qy 601 CAGAGGGCTGCGCGCCAGCGCGGGGCGCAGTGACACAGAGGGGCTGGACTTCGCT 660
Db 601 CAGAGGGCTGCGCGCCAGCGCGGGGCGCAGTGACACAGAGGGGCTGGACTTCGCT 660
Qy 661 GTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTTCTGTCTGCTG 720
Db 661 GTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTTCTGTCTGCTG 720
Qy 721 TTATCACCTTTACTGCAACACAGGACCGAAGCGTTTGGAAATGTCCTCCCGGCTG 780
Db 721 TTATCACCTTTACTGCAACACAGGACCGAAGCGTTTGGAAATGTCCTCCCGGCTG 780
Qy 781 TGGTCAAAATCGGAGACAAGCCAGCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAGCCAGCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG 840
Qy 841 CCATCATATTTACTTCAACTGAGATCTCTTCTTTAGGGAGCAAGTCTTCCCTTTCAT 900
Db 841 CCATCATATTTACTTCAACTGAGATCTCTTCTTTAGGGAGCAAGTCTTCCCTTTCAT 900
Qy 901 TTTTTCAGTCTTCTCCCTGTGATTTCAATCTCATGATTTATTTTAGTGGGCGCGG 960
Db 901 TTTTTCAGTCTTCTCCCTGTGATTTCAATCTCATGATTTATTTTAGTGGGCGCGG 960
Qy 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGGACGGGAAACAAACTAGGTAAATCTTAC 1020
Db 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGGACGGGAAACAAACTAGGTAAATCTTAC 1020

Db 961 GTGGGAAGATTAATCTTTTCTTTATGTGTTTGAACGGAACAAAACTAGGTAAAACTTAC 1020
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Db 1021 AGTACACCAAGGGTCAACAATACTGTGTGCGCACATCGCGTAGGGCTGAAAGGGG 1080
QY 1081 CAGGCCAGAGTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGAGGCGACCCATG 1140
Db 1081 CAGGCCAGAGTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGAGGCGACCCATG 1140
QY 1141 CATCTCTCAACCTCTTCCCGCCCGTTTACAAAGGGGGAGGCTTAAGCCCGAGAGCAGCT 1200
Db 1141 CATCTCTCAACCTCTTCCCGCCCGTTTACAAAGGGGGAGGCTTAAGCCCGAGAGCAGCT 1200
QY 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTAGCTGAGGGAACCTTGTCTCCCA 1260
Db 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTAGCTGAGGGAACCTTGTCTCCCA 1260
QY 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTTCTTTTCCGAGGCCCTGTCTCAGGG 1320
Db 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTTCTTTTCCGAGGCCCTGTCTCAGGG 1320
QY 1321 TGAGGTGCTTGAGTCTCCACGCGAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT 1380
Db 1321 TGAGGTGCTTGAGTCTCCACGCGAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT 1380
QY 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT 1440
Db 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT 1440
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCTAAATTTGATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCTAAATTTGATAGACCTAA 1500
QY 1501 AATATAAAGTGGTGGCTTAAACCTGGAATGAATCCCTCTATCTCTTAAGAAAT 1560
Db 1501 AATATAAAGTGGTGGCTTAAACCTGGAATGAATCCCTCTATCTCTTAAGAAAT 1560
QY 1561 CTCTGTGAACCCCTATGTGGAGGGCGAATGTCTCTCCAGGCCCTTGCAATGCGAGGGG 1620
Db 1561 CTCTGTGAACCCCTATGTGGAGGGCGAATGTCTCTCCAGGCCCTTGCAATGCGAGGGG 1620
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTAGGTTAAA 1680
QY 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATCA 1740
Db 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATCA 1740
QY 1741 CTTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT 1800
Db 1741 CTTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT 1800
QY 1801 CAACTAGCAGATACAGGGATGAGGACACCTGACTCTCTTAAAGGAGGCTGAGAGGCCAAA 1860
Db 1801 CAACTAGCAGATACAGGGATGAGGACACCTGACTCTCTTAAAGGAGGCTGAGAGGCCAAA 1860
QY 1861 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGATAGTATGATAGCAATGCTGCCATT 1920
Db 1861 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGATAGTATGATAGCAATGCTGCCATT 1920
QY 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATATCTTCCACCTTAGG 1980
Db 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATATCTTCCACCTTAGG 1980
QY 1981 AATAATCTCCTGTTAATATGTTGATCAATTTCTTCTGATTTATTTTCTACACATACATGTA 2040
Db 1981 AATAATCTCCTGTTAATATGTTGATCAATTTCTTCTGATTTATTTTCTACACATACATGTA 2040
QY 2041 AATATGCTCTTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAAT 2100
Db 2041 AATATGCTCTTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAAT 2100

QY 2101 AAACATTTTAGCATCTCTTTAAATGGTAAACAGCAAAAAA 2160
Db 2101 AAACATTTTAGCATCTCTTTAAATGGTAAACAGCAAAAAA 2160
QY 2161 AAAAAA 2220
Db 2161 AAAAAA 2220
QY 2221 AAAAAA 2261
Db 2221 AAAAAA 2261

RESULT 5

ID AD226401 standard; cDNA; 2261 BP.

XX AD226401;

AC AD226401;

DT 16-JUN-2005 (first entry)

XX Human CD8 cDNA.

DE cell culture; stem cell; CD8; ss; gene.

XX Homo sapiens.

XX WO2005030999-A1.

XX 07-APR-2005.

XX 24-SEP-2004; 2004WO-US031524.

PR 25-SEP-2003; 2003US-0506221P.

PR 08-OCT-2003; 2003US-0509594P.

XX (DAND) DANA FARBER CANCER INST INC.

XX Ritz J, Wu CJ;

DR WPI; 2005-273394/28.

DR P-PSDB; AD226402.

XX
PT Detecting lineage-specific cells in a biological sample, useful for determining the clinical outcome of a progenitor cell transfer in a subject, comprises identifying lineage-specific mRNA in the sample.
XX
PS Disclosure; SEQ ID NO 27; 393pp; English.
XX
CC The invention relates to a method of detecting lineage-specific cells in a biological sample which comprises identifying lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents a human cDNA that encodes a protein used to identify lineage-specific cells.

XX
SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 14; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAGGCTCCGGGCGGCGGAAGGCGCAACTTTCCCTCGGCGCCCAACCGGCT 60
Db 1 GAAATCAGGCTCCGGGCGGCGGAAGGCGCAACTTTCCCTCGGCGCCCAACCGGCT 60
QY 61 CCCGCGCCCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCGCTCTGGGAGCGGTCA 120
Db 61 CCCGCGCCCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCGCTCTCTGGGAGCGGTCA 120
QY 121 TGGCCTTACAGTGAGCCGCTTGTCTCCCTGCGCTTGTCTCCAGCGCGCAGGC 180

N6 - Jute

Db 121 TGGCCTTACCAAGTACCGCCCTTGCTCTGCGCTGGCCCTTGCTGCTCACGCCGCCAGGC 180
Qy 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAGC 240
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Db 241 TGAATGTCAGGTCGTGCTGTCGAACCCGACGTCGGGCTGCTGCTGGGCTTCACAGCGC 300
Qy 301 GCGGCGCGCGCAGTCCCACTCTCTCTATACCTCTCCCAAAACGAGCCCAAGGCGG 360
Db 301 GCGGCGCGCGCAGTCCCACTCTCTCTATACCTCTCCCAAAACGAGCCCAAGGCGG 360
Qy 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGACACCTTCGCTCTCA 420
Db 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGACACCTTCGCTCTCA 420
Qy 421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Db 421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Qy 481 CCATCATGTACTCAGCCACTTCGTGCGGCTCTCTGCGAGCGAAGCCACACGAGCG 540
Db 481 CCATCATGTACTCAGCCACTTCGTGCGGCTCTCTGCGAGCGAAGCCACACGAGCG 540
Qy 541 CAGCGCCGCGACCAACACCGCGGCCACCATCGCGTCGAGCCCTGCTCGGCC 600
Db 541 CAGCGCCGCGACCAACACCGCGGCCACCATCGCGTCGAGCCCTGCTCGGCC 600
Qy 601 CAGAGGCTGCGCGCAGCGCGGGGGCGAGTGCAACAGAGGGGGTGACCTTCGCT 660
Db 601 CAGAGGCTGCGCGCAGCGCGGGGGCGAGTGCAACAGAGGGGGTGACCTTCGCT 660
Qy 661 GTGATATCTACCTGCGCGCCCTGCGCGGACTTGTGGGCTCTCTCTGCTGCACTGG 720
Db 661 GTGATATCTACCTGCGCGCCCTGCGCGGACTTGTGGGCTCTCTCTGCTGCACTGG 720
Qy 721 TTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAATGTCCCGGCTG 780
Db 721 TTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAATGTCCCGGCTG 780
Qy 781 TGGTCAAAATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAG 840
Qy 841 CCACCTACATTTACTCAAACTGAGATCCTCTCTTTTGGGAGCAAGTCTTCCCTTTTCA 900
Db 841 CCACCTACATTTACTCAAACTGAGATCCTCTCTTTTGGGAGCAAGTCTTCCCTTTTCA 900
Qy 901 TTTTTCAGTCTTCTCCCTGTGATTCATCTCATGATTAATTTAGTGGGGCGGG 960
Db 901 TTTTTCAGTCTTCTCCCTGTGATTCATCTCATGATTAATTTAGTGGGGCGGG 960
Qy 961 GTGGAAAGATTAATTTTCTTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTAC 1020
Db 961 GTGGAAAGATTAATTTTCTTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTAC 1020
Qy 1021 AGTACACCAAGGTCACATCTGTTGCGCACATCGCGTAGGCGTGGAAAGGG 1080
Db 1021 AGTACACCAAGGTCACATCTGTTGCGCACATCGCGTAGGCGTGGAAAGGG 1080
Qy 1081 CAGGCGAGGCTACCCGCGAGAGTTCTCAGAACTCATGCTGAGAGAGCTGGAGCACCATG 1140
Db 1081 CAGGCGAGGCTACCCGCGAGAGTTCTCAGAACTCATGCTGAGAGAGCTGGAGCACCATG 1140
Qy 1141 CCATCTCAACTCTTCCCGCGCGTTCCTCAAAAGGGGAGGCTAAAGCCGAGAGCAGCT 1200
Db 1141 CCATCTCAACTCTTCCCGCGCGTTCCTCAAAAGGGGAGGCTAAAGCCGAGAGCAGCT 1200
Qy 1201 TGATCAAAAGGCACACAGCAAGTCAGGTTTGGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260

Db 1201 TGATCAAAAGGCACACAGCAAGTCAGGTTTGGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
Qy 1261 GCTCAGGCTCTTTCTCCACACCATTCAGGTCTTTTCTTCCGAGGCCCTGTCTCAGGG 1320
Db 1261 GCTCAGGCTCTTTCTCCACACCATTCAGGTCTTTTCTTCCGAGGCCCTGTCTCAGGG 1320
Qy 1321 TGAGGTCTTGAGTCTCCNACGGCAAGGAACAGTACTTCTTGATACCTGGGATACGT 1380
Db 1321 TGAGGTCTTGAGTCTCCNACGGCAAGGAACAGTACTTCTTGATACCTGGGATACGT 1380
Qy 1381 GCCCAGAGCCTCCGAGGAGTAATGAATTAAGAAAGAGAACTGCCCTTTGGCAGAGTCTAT 1440
Db 1381 GCCCAGAGCCTCCGAGGAGTAATGAATTAAGAAAGAGAACTGCCCTTTGGCAGAGTCTAT 1440
Qy 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGTATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGTATAGACCTAA 1500
Qy 1501 AATAAATGAAGTGGTGAAGCTTAACCTGGAAATGAATCCCTCTATCTTAAAGAAAT 1560
Db 1501 AATAAATGAAGTGGTGAAGCTTAACCTGGAAATGAATCCCTCTATCTTAAAGAAAT 1560
Qy 1561 CTCTGTGAACCCCTATGTGGAGCGGAATGTCTCTCCAGCCCTTGCAATTCAGAGGG 1620
Db 1561 CTCTGTGAACCCCTATGTGGAGCGGNAATGTCTCTCCAGCCCTTGCAATTCAGAGGG 1620
Qy 1621 CCCATGAAGAGGACAGGCTAACCCCTTTTACAATAGAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTAACCCCTTTTACAATAGAATTTGAGCATCAGTGAGGTTAAA 1680
Qy 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAACATGTTCTCGGATCACTGATGA 1740
Db 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAACATGTTCTCGGATCACTGATGA 1740
Qy 1741 CTTTATTAATCTTTGTAAGACAAATTTGGAGAGCCCTCACACAGCCCTGGCCCTCTGCT 1800
Db 1741 CTTTATTAATCTTTGTAAGACAAATTTGGAGAGCCCTCACACAGCCCTGGCCCTCTGCT 1800
Qy 1801 CAACTAGCAGATACAGGATGAGGACACCTGACTCTCTTTAAGAGGCTGAGAGCCCAA 1860
Db 1801 CAACTAGCAGATACAGGATGAGGACACCTGACTCTCTTTAAGAGGCTGAGAGCCCAA 1860
Qy 1861 CTGCTGTCCCAACATGCACTCTCTTAAAGTATGTTAAGCAATGCTGCCCCAT 1920
Db 1861 CTGCTGTCCCAACATGCACTCTCTTAAAGTATGTTAAGCAATGCTGCCCCAT 1920
Qy 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCCACTATAATTTCTTCCCTTAGG 1980
Db 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCCACTATAATTTCTTCCCTTAGG 1980
Qy 1981 AATAATCTCTGTTAATAATGTTGATCTTCTGATATTTTCTACACATATGTA 2040
Db 1981 AATAATCTCTGTTAATAATGTTGATCTTCTGATATTTTCTACACATATGTA 2040
Qy 2041 AATATGCTTTCTTTTTTAAATAGGTTGATCTATGCTTATGATGCTTTTAAATGAT 2100
Db 2041 AATATGCTTTCTTTTTTAAATAGGTTGATCTATGCTTATGATGCTTTTAAATGAT 2100
Qy 2101 AAAATTTGTAGCTCTCTTTTAAATAGGTAACAGCAAAAAAAGGAAAAAAGG 2160
Db 2101 AAAATTTGTAGCTCTCTTTTAAATAGGTAACAGCAAAAAAAGGAAAAAAGG 2160
Qy 2161 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2220
Db 2161 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2220
Qy 2221 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2261
Db 2221 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2261


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Db 2293 G C C C A G A G C C T C G A G G A G G T A A T G A A T T A A A G A G A G A A C T G C C T T T T G C G A G A G T T C T A T 2352
Qy 1441 A A T G T A A C A A T A T C A G A C T T T T T T T T T T T T T T T T T T A T A T C A A G C C T A A A A T T G T A T A G A C C T A A 1500
Db 2353 A A T G T A A C A A T A T C A G A C T T T T T T T T T T T T T T T T T T A T A T C A A G C C T A A A A T T G T A T A G A C C T A A 2412
Qy 1501 A A T A A A T G A A G T G A G C T T A A C C C T G G A A A A T G A A T C C C T A T C T A T C T T A A A G A A A T 1560
Db 2413 A A T A A A T G A A G T G A G C T T A A C C C T G G A A A A T G A A T C C C T A T C T A T C T T A A A G A A A T 2472
Qy 1561 C T C T G T G A A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1620
Db 2473 C T C T G T G A A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 2532
Qy 1621 C C C A T G A A G A G G A C A G C T A C C C C T T T A C A A A T A G A A T T T G A G C A T C A G T G A G G T T A A A 1680
Db 2533 C C C A T G A A G A G G A C A G C T A C C C C T T T A C A A A T A G A A T T T G A G C A T C A G T G A G G T T A A A 2592
Qy 1681 C T A A G G C C C T C T T G A A T C T T G A A T T T G A G A T A C A A A C A T G T T C T G G A T C A C T G A T G A 1740
Db 2593 C T A A G G C C C T C T T G A A T C T C T G A A T T T G A G A T A C A A A C A T G T T C T G G A T C A C T G A T G A 2652
Qy 1741 C T T T T T A T A C T T T T A A G A C A A T T T T G G A G C C C C T C A C A G C C C T G C C T G C T G C T 1800
Db 2653 C T T T T T A T A C T T T T A A G A C A A T T T T T G G A G C C C C T C A C A G C C C T G C C T G C T G C T 2712
Qy 1801 C A A C T A G C A G A T A C A G G A T A G G C A G C A C C T G A C T C T C T T A A G A G G C T G A G A G C C C A A A 1860
Db 2713 C A A C T A G C A G A T A C A G G A T A G G C A G C A C C T G A C T C T C T T A A G A G G C T G A G A G C C C A A A 2772
Qy 1861 C T G C T G T C C C A A A C A T G C A C T T C C T T G T T A A G T A T G G T A C A A G C A A T G C T G C C C A A T 1920
Db 2773 C T G C T G T C C C A A A C A T G C A C T T C C T T G C T T A A G T A T G T T A C A A G C A A T G C C T G C C A A T 2832
Qy 1921 G G A G A A A A A C T T A A G T A G A T A A G A A A T A A G A C C A C T A T A A T T C T T C A C C T T A G G 1980
Db 2833 G G A G A A A A A C T T A A G T A G A T A A G A A A T A A G A A C C A C T A T A A T T C T T C A C C T T A G G 2892
Qy 1981 A A T A A T C C C T G T T A A T A T G T G T A C A T T C T T C C T G A T T A T T T C T A C A C A T A C A T G T A A 2040
Db 2893 A A T A A T C C C T G T T A A T A T G T G T A C A T T C T C T G A T A T T T T C T A C A C A T A C A T G T A A 2952
Qy 2041 A A T A T G C T T T T T T T T A A A T A G G G T T G T A C T A T G C T G T T A T A G T A G C G C T T T A A T G A A T 2100
Db 2953 A A T A T G C T T T T T T T T A A A T A G G G T T G T A C T A T G C T G T T A T A G T A G C G C T T T A A T G A A T 3012
Qy 2101 A A A C A T T T G T A G C A T C C T C T T T A A T G G G T A A A C A G C 2136
Db 3013 A A A C A T T T G T A G C A T C C T C T T T A A T G G G T A A A C A G C 3048
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RESULT 7

ID ADQ22926 standard; DNA; 2134 BP.

AC ADQ22926;

XX ADQ22926;

XX 26-AUG-2004 (first entry)

DT Human soft tissue sarcoma-upregulated DNA - SEQ ID 5746.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

DE ds.

XX Homo sapiens.

XX OS

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
PA Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX Example 2; SEQ ID NO 5746; 210pp; English.
PS The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cyostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX Sequence 2134 BP; 539 A; 586 C; 515 G; 494 T; 0 U; 0 Other;
SQ

Query Match 91.2%; Score 2061.6; DB 12; Length 2134;
Best Local Similarity 97.7%; Pred. No. 1.7e-280;
Matches 2130; Conservative 0; Mismatches 4; Indels 46; Gaps 2;
Qy 1 G A A T C A G G C T C C G G G C G G C G A A G G G C G A A C T T T C C C C C C C C G G C G C C C A C C G C T 60
Db 1 G A A T C A G G C T C C G G G C G G C G G C C G A A G G G C G A A C T T T C C C C C C C C G G C G C C C A C C G C T 60
Qy 61 C C C C G G G C C T C C C C T C G C G C C C G A G C T T C A G A C C A A G C A G C G T C C T G G G A G C G C G T C A 120
Db 61 C C C C G G G C C T C C C C T C G G G C C C G A G C T T C A G A C C A A G C A G C G T C C T G G G A G C G C G T C A 120
Qy 121 T G G C C T A C A G T G A C C G C C T T G C T C C G C T G G C C T T G C T C C A C G C C C C A G C G C 180
Db 121 T G G C C T A C A G C A C G C C T T G C T C C G C G C T G C T C C A C G C C C C A G C G C C C A G C G C 180
Qy 181 C G A G C C A G T T C C G G G T G C G C G C C T G G A C C T G G A A C C T G G G C G A G A C A G T G G A G C 240
Db 181 C G A G C C A G T T C C G G G T G C G C G C C T G G A C C T G G A A C C T G G G C G A G A C A G T G G A G C 240
Qy 241 T G A A G T C C A G G T G C T G T C C A A C C G A C T G G G G T G C T G C T G G G T C T T T C C A G C C G C 300
Db 241 T G A A G T C C A G G T G C T G T C C A A C C G A C G T C G G G C T G C T G C T G G G T C T T T C C A G C C G C 300
Qy 301 G C G G C G C G C G C C A G T C C C A C C T T C C T A T A C T C T C C C A A A A A A A G C C C A A G C G G G 360
Db 301 G C G G C G C G C G C C A G T C C C A C C T T C C T A T A C T C T C C C A A A A A A A G C C C A A G C G G G 360
Qy 361 C C G A G G G C T G G A C A C C C A G C G G T T C T C G G G C A A G A G G T T G G G G A C A C C T T C G T C C T C A 420
Db 361 C C G A G G G C T G G A -----CA 375
Qy 421 C C C T G A G C G A C T T C C G C G A G A A C A G A G G C T A C T A T T T C T G C T G C G C C C T G A G C A A C T 480
Db 376 C C C T G A G C G A C T T C C G C G A G A A C A G A G G C T A C T A T T T C T G C T G C G C C C T G A G C A A C T 435
Qy 481 C C A T C A T G T A C T T C A G C C A C T T G C G C G G T C C T G C C A G C G A A G C C C A C C A C A C G C G C 540
Db 436 C C A T C A T G T A C T T C A G C C A C T T C G T G C C G G T C T T C C T G C C A G C G A A G C C C A C C A C G C G C 495
Qy 541 C A G C G C G C G A C C A C C A C C G G C C C A C C A T C G C G T C G C A G C C C C T G T C C C T G C G C G C 600

| | | | |
|------|----|--|------|
| 496 | Db | CAGCGCCGCGACCAACCAACCGGGGCCCAACATCGCGTGCAGCCCTGTCTCTGCGCC | 555 |
| 601 | Qy | CAGAGCGGTGCGGCGCAAGCGCGGGGGCGCAGTGCACACAGAGGGGCTGCATTTCCGCT | 660 |
| 556 | Db | | 615 |
| 661 | Qy | GTGATATCTACATCTGGGCGCCCTTGGCGGGACCTTGTGGGGTCCCTTCTCTCTGTCACTGG | 720 |
| 616 | Db | GTGATATCTACATCTGGGCGCCCTTGGCGGGACCTTGTGGGGTCCCTTCTCTCTGTCACTGG | 675 |
| 721 | Qy | TTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCGCCGCGCTG | 780 |
| 676 | Db | TTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCGCCGCGCTG | 735 |
| 781 | Qy | TGGTCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 840 |
| 736 | Db | TGGTCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 795 |
| 841 | Qy | CCACTACATTACTTCAAACCTGAGATCCCTTTTGTAGGGAGCAAGTCCCTTCCTTTTCAT | 900 |
| 796 | Db | CCACTACATTACTTCAAACCTGAGATCCCTTTTGTAGGGAGCAAGTCCCTTCCTTTTCAT | 855 |
| 901 | Qy | TTTTTTTCAGTCTTCCCTCCCTGTGATTTCAATCTCATGATTAATTATTTTAGTGGGGGGG | 960 |
| 856 | Db | TTTTTTTCAGTCTTCCCTCCCTGTGATTTCAATCTCATGATTAATTATTTTAGTGGGGGGG | 915 |
| 961 | Qy | GTGGAAAGATTACTTTTTTTCTTATGTGTTTGACGGGAAACAAACCTAGTAAAACTCTAC | 1020 |
| 916 | Db | GTGGAAAGATTACTTTTTTTCTTATGTGTTTGACGGGAAACAAACCTAGTAAAACTCTAC | 975 |
| 1021 | Qy | AGTACACCAAGGGTCACAATACTGTGTGTGCGCACATCGCGTAGGGCTGTGAAAGGGG | 1080 |
| 976 | Db | AGTACACCAAGGGTCACAATACTGTGTGTGCGCACATCGCGTAGGGCTGTGAAAGGGG | 1035 |
| 1081 | Qy | CAGCCAGAGCTACCCGACAGTCTCAGAACTCATGCTGAGAGAGCTGGAGGACCCCATG | 1140 |
| 1036 | Db | CAGCCAGAGCTACCCGACAGTCTCAGAACTCATGCTGAGAGAGCTGGAGGACCCCATG | 1095 |
| 1141 | Qy | CCATCTCAACCTCTTCCCGCCCGCTTTTACAAGGGGGAGGCTAAAGCCACAGAGACAGCT | 1200 |
| 1096 | Db | CCATCTCAACCTCTTCCCGCCCGCTTTTACAAGGGGGAGGCTAAAGCCACAGAGACAGCT | 1155 |
| 1201 | Qy | TGATCAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| 1156 | Db | TGATCAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1215 |
| 1261 | Qy | GCTCAGGGCTCTTCTCTCCACACATTCAGGTCCTTCTTCGAGGGCCCTGTCTCAGGG | 1320 |
| 1216 | Db | GCTCAGGGCTCTTCTCTCCACACATTCAGGTCCTTCTTCGAGGGCCCTGTCTCAGGG | 1275 |
| 1321 | Qy | TGAGGTGCTTGAGTCTCCACGGCAAGGAAACAGTACTCTTCTGATACCTGGGATACTGT | 1380 |
| 1276 | Db | TGAGGTGCTTGAGTCTCCACGGCAAGGAAACAGTACTCTTCTGATACCTGGGATACTGT | 1335 |
| 1381 | Qy | GCCCAGAGCCTCGAGGAGGTAAATGAAATTAAGAGAGAACTGCTTTGGCAGAGTCTCTAT | 1440 |
| 1336 | Db | GCCCAGAGCCTCGAGGAGGTAAATGAAATTAAGAGAGAACTGCTTTGGCAGAGTCTCTAT | 1395 |
| 1441 | Qy | AATGTAACAATATCAGACTTTTTTTTTTTTATTAATCAAGCCTAAAAATGATAGACCTAA | 1500 |
| 1396 | Db | AATGTAACAATATCAGAC-TTTTTTTTTTTTATTAATCAAGCCTAAAAATGATAGACCTAA | 1454 |
| 1501 | Qy | AATAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTTAAGAAAT | 1560 |
| 1455 | Db | | 1514 |
| 1561 | Qy | CTCTGTGAAAACCCCTATGTGTGAGCGGAAATGTCTCTCCAGCCCTTGCAATGCAGAGGGG | 1620 |
| 1515 | Db | CTCTGTGAAAACCCCTATGTGTGAGCGGAAATGTCTCTCCAGCCCTTGCAATGCAGAGGGG | 1574 |
| 1621 | Qy | CCCATGAAAGAGGACAGGCTACCCCTTTTACAATAGAAATTTGAGCAATCAGTGAAGTTAAA | 1680 |
| 1575 | Db | CCCATGAAAGAGGACAGGCTACCCCTTTTACAATAGAAATTTGAGCAATCAGTGAAGTTAAA | 1634 |

| | | | |
|----------|--|---|------|
| Qy | 1681 | CTAAGGCCCTCTGGAATCTCTCGAATTGGAGATACAAACATGTTCCTGGGATCACTGATGA | 1741 |
| Db | 1635 | CTAAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTCCTGGGATCACTGATGA | 1694 |
| Qy | 1741 | CTTTTTATACTTTTGAAGAACAATTGTGGAGAGCCCTCACACAGCCCTGGCCTCTGCCT | 1800 |
| Db | 1695 | CTTTTTATACTTTTGAAGAACAATTGTGGAGAGCCCTCACACAGCCCTGGCCTCTGCCT | 1754 |
| Qy | 1801 | CAACTAGCAGATACAGGGATGAGGCAGACCTGACTCTCTTTAAGGAGGCTGAGAGCCCCAAA | 1860 |
| Db | 1755 | CAACTAGCAGATACAGGGATGAGGCAGACCTGACTCTCTTTAAGGAGGCTGAGAGCCCCAAA | 1814 |
| Qy | 1861 | CTGCTGTCCTCCAAACATGCATCTCTTGCTTAAGGTATGGTACAGCAATGCCTGCCCAT | 1920 |
| Db | 1815 | CTGCTGTCCTCCAAACATGCATCTCTTGCTTAAGGTATGGTACAGCAATGCCTGCCCAT | 1874 |
| Qy | 1921 | GGAGAGAAAAAACCTTTAGTAGATAAGGAAATAAGAACCACTCATATAATCTTCAACCTTAGG | 1980 |
| Db | 1875 | GGAGAGAAAAAACCTTTAGTAGATAAGGAAATAAGAACCACTCATATAATCTTCAACCTTAGG | 1934 |
| Qy | 1981 | AATAATCTCTGTTAAATPANGGTGTACATCTTCTCGATTATTTTCTACACATACATGTAA | 2040 |
| Db | 1935 | AATAATCTCTGTTAAATPANGGTGTACATCTTCTCGATTATTTTCTACACATACATGTAA | 1994 |
| Qy | 2041 | AATATGTCCTTCTTTTAAATAGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT | 2100 |
| Db | 1995 | AATATGTCCTTCTTTTAAATAGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT | 2054 |
| Qy | 2101 | AAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2160 |
| Db | 2055 | AAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2114 |
| Qy | 2161 | AAAAAAAAAAAAAAAAAAAAA 2180 | |
| Db | 2115 | AAAAAAAAAAAAAAAAAAAAA 2134 | |
| RESULT 8 | | | |
| ADF90782 | | | |
| ID | ADF90782 standard; DNA; 2123 BP. | | |
| XX | | | |
| AC | ADF90782; | | |
| XX | | | |
| DT | 26-FEB-2004 (first entry) | | |
| XX | | | |
| DE | Human hepatic-fibrosis disease marker SEQ ID 244. | | |
| XX | | | |
| KW | Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis; | | |
| KW | hepatic carcinoma; human; ds. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | JP2003259877-A. | | |
| XX | | | |
| PD | 16-SEP-2003. | | |
| XX | | | |
| PF | 11-MAR-2002; 2002JP-00065013. | | |
| XX | | | |
| PR | 11-MAR-2002; 2002JP-00065013. | | |
| XX | | | |
| PA | (SUMU) SUMITOMO SEIYAKU KK. | | |
| XX | | | |
| DR | WPI; 2003-821598/77. | | |
| XX | | | |
| PT | Hepatic fibrosis disease markers comprising polynucleotides or antibodies, useful for improved diagnosis, screening and developing drugs to treat hepatitis, to control cirrhosis and carcinoma. | | |
| PT | | | |
| XX | | | |
| FS | Claim 1; SEQ ID NO 244; 313pp; Japanese. | | |
| XX | | | |
| CC | The present invention relates to hepatic-fibrosis disease markers (ADP90539-ADP90871) and related proteins (ADP90872-ADP90917). The | | |
| CC | | | |

CC sequences are useful for detecting and treating hepatic fibrosis caused
CC by alcohol consumption, virus infection, etc., and the associated chronic
CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
CC precision), so more suitable treatments can be developed and given.
XX

SQ Sequence 2123 BP; 508 A; 586 C; 528 G; 501 T; 0 U; 0 Other;

Query Match 91.2%; Score 2061.2; DB 10; Length 2123;

Best Local Similarity 99.8%; Pred. No. 2e-280;

Matches 2075; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

| | | | |
|----|-----|---|------|
| Qy | 45 | CGGCGCCCAACCGGCTCCGGCGCGCTCCCTCCGCGCCCGAGCTTCGAGCCAAACGAGGT | 104 |
| Db | 6 | CGGCGCCCAACCGGCTCCGGCGCGCTCCCTCCGCGCCCGAGCTTCGAGCCAAACGAGGT | 65 |
| Qy | 105 | CCTGGGAGCGCTCATGCGCTTACAGTACCGCTTGTCTCTCCGCTGGCTTGTCTG | 164 |
| Db | 66 | CCTGGGAGCGCTCATGCGCTTACAGTACCGCTTGTCTCTCCGCTGGCTTGTCTG | 125 |
| Qy | 165 | CTCACGCGCGCAGCGCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGAAACCTG | 224 |
| Db | 126 | CTCACGCGCGCAGCGCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGAAACCTG | 185 |
| Qy | 225 | GGCGAGACAGTGGAGCTGAAGTGCAGGTGTCTGTCTCAACCGGAGTGGGCTGTCTG | 284 |
| Db | 186 | GGCGAGACAGTGGAGCTGAAGTGCAGGTGTCTGTCTCAACCGGAGTGGGCTGTCTG | 245 |
| Qy | 285 | TGGCTCTTCCAGCGCGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAA | 344 |
| Db | 246 | TGGCTCTTCCAGCGCGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAA | 305 |
| Qy | 345 | AACAGCCCAAGCGCGCGCGCGCGCGCGGTTCGCGGCAAGAGGTGGGG | 404 |
| Db | 306 | AACAGCCCAAGCGCGCGCGCGCGCGGTTCGCGGCAAGAGGTGGGG | 365 |
| Qy | 405 | GACACCTTGTCTCACCTGAGGACCTTCGCGCGAGAGAACGAGGGCTACTATTTCTGC | 464 |
| Db | 366 | GACACCTTGTCTCACCTGAGGACCTTCGCGCGAGAGAACGAGGGCTACTATTTCTGC | 425 |
| Qy | 465 | TCGGCCTTGACCACTCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCGCAGCG | 524 |
| Db | 426 | TCGGCCTTGACCACTCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCGCAGCG | 485 |
| Qy | 525 | AAGCCCAACAGCGCGCGCGCGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAG | 584 |
| Db | 486 | AAGCCCAACAGCGCGCGCGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAG | 545 |
| Qy | 585 | CCCTGTCTCCCTGGCGCGAGCGGTGCGCGCGCGCGCGCGCGCGAGTGCACACGAGG | 644 |
| Db | 546 | CCCTGTCTCCCTGGCGCGAGCGGTGCGCGCGCGCGCGCGCGCGAGTGCACACGAGG | 605 |
| Qy | 645 | GGGCTGGACTTCGCTGTGATATCTACATCTGGGCGCGCTTCGGCGCGACTTGTGGGGTC | 704 |
| Db | 606 | GGGCTGGACTTCGCTGTGATATCTACATCTGGGCGCGCTTCGGCGCGACTTGTGGGGTC | 665 |
| Qy | 705 | CTTCTCTGTCACTGGTTATCACCTTTACTGCAACCAAGAGAACCGGAGACGTGTTTCG | 764 |
| Db | 666 | CTTCTCTGTCACTGGTTATCACCTTTACTGCAACCAAGAGAACCGGAGACGTGTTTCG | 725 |
| Qy | 765 | AAATGTCCCGCGCTGTGGTCAATTCGGGAGACAGCCAGCCCTTCGGCGAGATACGTC | 824 |
| Db | 726 | AAATGTCCCGCGCTGTGGTCAATTCGGGAGACAGCCAGCCCTTCGGCGAGATACGTC | 785 |
| Qy | 825 | TAACTCTGTCAACAGCCACTACATTAATCAAACTGAGATCCTTCTTTTGGGAGCA | 884 |
| Db | 786 | TAACTCTGTCAACAGCCACTACATTAATCAAACTGAGATCCTTCTTTTGGGAGCA | 845 |
| Qy | 885 | AGTCTTCCCTTTCAATTTTTCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT | 944 |
| Db | 846 | AGTCTTCCCTTTCAATTTTTCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT | 905 |
| Qy | 945 | TTTTAGTGGGGCGGGTGGGAAAGATTACTTTTTTTTATGTGTTTGACGGGAAACAA | 1004 |

| | | | |
|----|------|--|------|
| Db | 906 | TTTTAGTGGGGCGGGTGGGAAAGATTACTTTTTTTTATGTGTTTGACGGGAAACAA | 965 |
| Qy | 1005 | ACTAGGTAATAATCTACAGTACACCAAGGCTACAATACTGTGTGTGGCAGCATCGCGGT | 1064 |
| Db | 966 | ACTAGGTAATAATCTACAGTACACCAAGGCTACAATACTGTGTGTGGCAGCATCGCGGT | 1025 |
| Qy | 1065 | AGGCGTGGAAAAGGGGAGGCGAGAGCTACCCGAGAGTTCTCAGATCATGCTGAGAGA | 1124 |
| Db | 1026 | AGGCGTGGAAAAGGGGAGGCGAGAGCTACCCGAGAGTTCTCAGATCATGCTGAGAGA | 1085 |
| Qy | 1125 | GCTGGAGGCAACCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTA | 1184 |
| Db | 1086 | GCTGGAGGCAACCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTA | 1145 |
| Qy | 1185 | AAGCCAGAGACAGCTTGTATCAAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGA | 1244 |
| Db | 1146 | AAGCCAGAGACAGCTTGTATCAAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGA | 1205 |
| Qy | 1245 | GGGACCTTGTCTCCAGCTCAGGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGA | 1304 |
| Db | 1206 | GGGACCTTGTCTCCAGCTCAGGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGA | 1265 |
| Qy | 1305 | GGCCCTGTCTCAGGGTGAAGTGTCTCAACGGCAAGGAAACAAGTACTTCTTG | 1364 |
| Db | 1266 | GGCCCTGTCTCAGGGTGAAGTGTCTCAACGGCAAGGAAACAAGTACTTCTTG | 1325 |
| Qy | 1365 | ATACCTGGGATPACTGTGCCAGAGCCTCGAGAGTAAATGAATTAAGAAGAGAACTGCC | 1424 |
| Db | 1326 | ATACCTGGGATPACTGTGCCAGAGCCTCGAGAGTAAATGAATTAAGAAGAGAACTGCC | 1385 |
| Qy | 1425 | TTTGGCAGAGTTCTAATGTAAACAATATCAGACTTTTTTTTTTTTATTAACAAGCCTAA | 1484 |
| Db | 1386 | TTTGGCAGAGTTCTAATGTAAACAATATCAGAC--TTTTTTTTTTATTAACAAGCCTAA | 1443 |
| Qy | 1485 | AAATGTATAGACCTAAATAAATAAGTGTGAGCTTAACCCCTGGAAAAATGAATCCCTC | 1544 |
| Db | 1444 | AAATGTATAGACCTAAATAAATAAGTGTGAGCTTAACCCCTGGAAAAATGAATCCCTC | 1503 |
| Qy | 1545 | TATCTCTAAAGAAAATCTCTGTGAAACCCCTATGTGGAGCGGAAATTCCTCTCCAGGCC | 1604 |
| Db | 1504 | TATCTCTAAAGAAAATCTCTGTGAAACCCCTATGTGGAGCGGAAATTCCTCTCCAGGCC | 1563 |
| Qy | 1605 | TTGCAATTCAGAGGGGCCATGAAAGAGGACAGGCTACCCCTTTTACAATTAAGATTGAG | 1664 |
| Db | 1564 | TTGCAATTCAGAGGGGCCATGAAAGAGGACAGGCTACCCCTTTTACAATTAAGATTGAG | 1623 |
| Qy | 1665 | CATCAGTGAGTTAAACTAAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTT | 1724 |
| Db | 1624 | CATCAGTGAGTTAAACTAAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTT | 1683 |
| Qy | 1725 | CTGGGATCAGTGAATTTTTTATCTTTGTAAGACAAATTTGAGAGAGCCCTCACAC | 1784 |
| Db | 1684 | CTGGGATCAGTGAATTTTTTATCTTTTATCTTTGTAAGACAAATTTGAGAGAGCCCTCACAC | 1743 |
| Qy | 1785 | AGCCCTGGCCTCTGCTCACTAGCAGATACAGGGATGAGGAGAGCCTGACTCTCTTAAGG | 1844 |
| Db | 1744 | AGCCCTGGCCTCTGCTCACTAGCAGATACAGGGATGAGGAGAGCCTGACTCTCTTAAGG | 1803 |
| Qy | 1845 | AGGCTGAGAGCCCAAACTGCTGCCAAACATGCACTTCTTCTTAAAGGTATGCTACAA | 1904 |
| Db | 1804 | AGGCTGAGAGCCCAAACTGCTGCCAAACATGCACTTCTTCTTAAAGGTATGCTACAA | 1863 |
| Qy | 1905 | GCAATGCTGCCATTTGGAGAGAAAACCTTAAAGTAGATAAGGAAATAAGAAACCACTCAT | 1964 |
| Db | 1864 | GCAATGCTGCCATTTGGAGAGAAAACCTTAAAGTAGATAAGGAAATAAGAAACCACTCAT | 1923 |
| Qy | 1965 | AAATCTTCCCTTTAGGAATAATCTCTGTTAAATGTTGATCATTTCTTCTGATATTTT | 2024 |
| Db | 1924 | AAATCTTCCCTTTAGGAATAATCTCTGTTAAATGTTGATCATTTCTTCTGATATTTT | 1983 |
| Qy | 2025 | CTACACATACATGTAAATAATGTCTTTTCTTTTAAATAGGGTGTGACTATCTGCTGATG | 2084 |

Db 1984 CTACATACATGTAATAATATGTCTTCTTTTAAATAGGGTTGTACTATGCTGTATG 2043

Qy 2085 AGTGGCTTTAATGAATPAACATTTGTAGCATCTCTTTAA 2124

Db 2044 AGTGGCTTTAATGAATPAACATTTGTAGCATCTCTTAAA 2083

RESULT 9

ADS92793

ID ADS92793 standard; cDNA; 2150 BP.

XX AC

XX ADS92793;

XX 16-DEC-2004 (first entry)

XX DE

XX cDNA of a secreted CD8 alpha-chain protein alternative transcript.

XX KW

XX immune response; cell-specific antigen; alloantigen; CD8;

XX KW

XX CD8 alpha-chain; cellular immune response; humoral immune response;

XX KW

XX transplant allograft; graft-versus-host disease; transplant; gene; ss.

XX OS

XX Homo sapiens.

XX FH

XX Key

XX Location/Qualifiers

XX CDS

XX 120..716

XX /*tag= a

XX /product= "CD8 alpha-chain"

XX FT

XX WO2004083244-A2.

XX PN

XX 30-SEP-2004.

XX PD

XX 19-MAR-2004; 2004WO-US008574.

XX PF

XX 19-MAR-2003; 2003US-0456378P.

XX PR

XX (ISOG-) ISOGENIS INC.

XX PA

XX Qi Y, Zhang X, Konigsberg PJ;

XX PI

XX WPI; 2004-691022/67.

XX DR

XX P-PSDB; ADS92792.

XX PS

XX Specifically inhibiting host immune responses to alloantigens, useful for

XX e.g. treating graft-versus-host disease, comprises contacting a target

XX cell expressing the antigen with an expression vector encoding a CD8

XX polypeptide.

XX Disclosure; Fig 1; 98pp; English.

XX CC

XX The specification describes a method for specifically inhibiting a host

XX immune response to target cell-specific antigens (e.g. alloantigens). The

XX method comprises contacting a target cell expressing the antigen with an

XX expression vector encoding a CD8 polypeptide comprising the CD8 alpha-

XX chain, where the CD8 polypeptide is expressed by the target cell and

XX where the host immune response against the target cell is specifically

XX inhibited. The method of the invention is useful for specifically

XX inhibiting both cellular and humoral immune responses to alloantigens,

XX thus finding use in extending the survival of transplant allografts and

XX in treating graft-versus-host disease in transplant recipients. The

XX present sequence encodes an alternative transcript of a secreted alpha-

XX chain of a CD8 protein. This CD8 alpha-chain may be used in the method of

XX the invention.

XX SQ

XX Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 89.7%; Score 2029; DB 13; Length 2150;

XX Matches 2150; Conservative 95.1%; Pred. No. 6.5e-276;

XX Mismatches 0; Indels 111; Gaps 1;

XX 1

XX GAAATCAGCTCCGGCGCGCGGCGAAGGGCGCAACTTCCCGCTCGGCGCCCCACCGCT 60

XX 1

XX GAAATCAGCTCCGGCGCGCGGCGAAGGGCGCAACTTCCCGCTCGGCGCCCCACCGCT 60

XX DB

Qy 61 CCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAGCAGCGTCTCTGGGAGCGCGTCA 120
Db 61 CCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAGCAGCGTCTCTGGGAGCGCGTCA 120
Qy 121 TGGCCTTACAGTGACCGGCTTGTCTCTGCGCGTGGCTTGTCTGCTCCACGCGCCAGGC 180
Db 121 TGGCCTTACAGTGACCGGCTTGTCTCTGCGCGTGGCTTGTCTGCTCCACGCGCCAGGC 180
Qy 181 CGAGCAGTTCGGGTGTGCGCGCTGGATCGAACCTGGAACTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCAGTTCGGGTGTGCGCGCTGGATCGAACCTGGAACTGGGCGAGACAGTGGAGC 240
Qy 241 TGAAGTGCAGGTGTGCTGTCTCCAAACCCGAGCTCGGGCTGTCTGCTGCTCTTCCAGCCGC 300
Db 241 TGAAGTGCAGGTGTGCTGTCTCCAAACCCGAGCTCGGGCTGTCTGCTGCTCTTCCAGCCGC 300
Qy 301 GGGCGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCTGCTCGGCGCTGAGCAACT 480
Db 301 GGGCGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCTGCTCGGCGCTGAGCAACT 480
Qy 301 GCGCGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCTGCTCGGCGCTGAGCAACT 480
Db 301 GCGCGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCTGCTCGGCGCTGAGCAACT 480
Qy 361 CCGAGGGCTGGACACCCAGCGGTTCGCGCAAGAGTGGGGGACACCTTCTGCTCTCA 420
Db 361 CCGAGGGCTGGACACCCAGCGGTTCGCGCAAGAGTGGGGGACACCTTCTGCTCTCA 420
Qy 421 CCTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAACT 480
Db 421 CCTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAACT 480
Qy 481 CCATCATGTATCTTCAAGCCACTTCTGTCGCGGTCTTCTGCGAGGAGCCACACGACGC 540
Db 481 CCATCATGTATCTTCAAGCCACTTCTGTCGCGGTCTTCTGCGAGGAGCCACACGACGC 540
Qy 541 CAGCGCGCGGACCAACACCGCGCGCCACCATCGCTCGCGAGCCCTGTCCTGCGCC 600
Db 541 CAGCGCGCGGACCAACACCGCGCGCCACCATCGCTCGCGAGCCCTGTCCTGCGCC 600
Qy 601 CAGAGCGTTCGCGCGCGCGCGCGAGTGCACACGAGGGGGCTGGACTTCGCGCT 660
Db 601 CAGAGCGTTCGCGCGCGCGCGCGAGTGCACACGAGGGGGCTGGACTTCGCGCT 660
Qy 661 GTGATATCTACATCTGGGCGCGCTTGGCGGGGCTTGTGGGGTCTTCTCTCTGCTCACTGG 720
Db 661 GTGATATCTACATCTGGGCGCGCTTGGCGGGGCTTGTGGGGTCTTCTCTCTGCTCACTGG 720
Qy 634 ----- 633
Db 634 ----- 633
Qy 721 TTATCACCTTTACTGCAACACACAGGAAACCGAGAGCTGTTTGCATAATGTCGCGCGCTG 780
Db 721 TTATCACCTTTACTGCAACACACAGGAAACCGAGAGCTGTTTGCATAATGTCGCGCGCTG 780
Qy 634 -----GGAACCGAGAGCTGTTTGCATAATGTCGCGCGCTG 669
Db 634 -----GGAACCGAGAGCTGTTTGCATAATGTCGCGCGCTG 669
Qy 781 TGGTCAAAATCGGGAGACAAGCCAGCCTTTTGGCGAGATACGCTCTAACCCCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGGAGACAAGCCAGCCTTTTGGCGAGATACGCTCTAACCCCTGTGCAACAG 840
Qy 841 CCATCATATTAATCTCAAACTGAGATCTTCTTTTGGAGGAGCAAGTCTTCCCTTTTCA 900
Db 841 CCATCATATTAATCTCAAACTGAGATCTTCTTTTGGAGGAGCAAGTCTTCCCTTTTCA 900
Qy 901 TTTTTCAGTCTCTCTCCCTGTATTCATCTCATGATATTATTTAGTGGGCGCGG 960
Db 901 TTTTTCAGTCTCTCTCCCTGTATTCATCTCATGATATTATTTAGTGGGCGCGG 960
Qy 790 TTTTTCAGTCTCTCTCCCTGTATTCATCTCATGATATTATTTAGTGGGCGCGG 849
Db 790 TTTTTCAGTCTCTCTCCCTGTATTCATCTCATGATATTATTTAGTGGGCGCGG 849
Qy 961 GTGGAAAGATTAATCTTTTCTTTTGTGTTTGGCGGAAACAAAACCTAGGTAAAACTTAC 1020
Db 961 GTGGAAAGATTAATCTTTTCTTTTGTGTTTGGCGGAAACAAAACCTAGGTAAAACTTAC 1020
Qy 850 GTGGAAAGATTAATCTTTTCTTTTGTGTTTGGCGGAAACAAAACCTAGGTAAAACTTAC 909
Db 850 GTGGAAAGATTAATCTTTTCTTTTGTGTTTGGCGGAAACAAAACCTAGGTAAAACTTAC 909
Qy 1021 AGTACACCAAGGGTCAAACTACTGTTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 1080
Db 1021 AGTACACCAAGGGTCAAACTACTGTTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 1080
Qy 910 AGTACACCAAGGGTCAAACTACTGTTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 969
Db 910 AGTACACCAAGGGTCAAACTACTGTTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 969
Qy 1081 CAGGCGAGAGTACCCGAGAGTCTCAGATCATGCTGAGAGAGCTGGAGGACCCCATG 1140
Db 1081 CAGGCGAGAGTACCCGAGAGTCTCAGATCATGCTGAGAGAGCTGGAGGACCCCATG 1140
Qy 970 CAGGCGAGAGTACCCGAGAGTCTCAGATCATGCTGAGAGAGCTGGAGGACCCCATG 1029
Db 970 CAGGCGAGAGTACCCGAGAGTCTCAGATCATGCTGAGAGAGCTGGAGGACCCCATG 1029

QY 1141 CCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCAGACAGCT 1200
Db |||||
QY 1030 CCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCAGACAGCT 1089
Db |||||
QY 1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1260
Db |||||
QY 1090 TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1149
Db |||||
QY 1261 GCTCAGGCTCTTCTCTCCACACCATTCAGTCTTTTTCCTCCGAGGCCCTGTCTCAGGG 1320
Db |||||
QY 1150 GCTCAGGCTCTTCTCTCCACACCATTCAGTCTTTTTCCTCCGAGGCCCTGTCTCAGGG 1209
Db |||||
QY 1321 TGAGGTGCTTACGCTCCAAAGGCAAGGACAGTACTTCTTATACCTGGGATCTGT 1380
Db |||||
QY 1210 TGAGGTGCTTACGCTCCAAAGGCAAGGACAGTACTTCTTATACCTGGGATCTGT 1269
Db |||||
QY 1381 GCCCAGAGCTCGAGGAGGTAAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Db |||||
QY 1270 GCCCAGAGCTCGAGGAGGTAAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1329
Db |||||
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAATTTGTATAGACCTAA 1500
Db |||||
QY 1330 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAATTTGTATAGACCTAA 1389
Db |||||
QY 1501 AATAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db |||||
QY 1390 AATAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1449
Db |||||
QY 1561 CTCTGTGAAACCCCTATCTGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCAGAGGGG 1620
Db |||||
QY 1450 CTCTGTGAAACCCCTATCTGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCAGAGGGG 1509
Db |||||
QY 1621 CCCATGAAGAGGACAGCTACCCCTTTTAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db |||||
QY 1510 CCCATGAAGAGGACAGCTACCCCTTTTAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1569
Db |||||
QY 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGATCACTGATGA 1740
Db |||||
QY 1570 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGATCACTGATGA 1629
Db |||||
QY 1741 CTTTATTATCTTTTAAAGACAATTTGTTGGAGAGCCCTTCACACAGCCCTGGCTCTGCT 1800
Db |||||
QY 1630 CTTTATTATCTTTTAAAGACAATTTGTTGGAGAGCCCTTCACACAGCCCTGGCTCTGCT 1689
Db |||||
QY 1801 CAACTAGCAGATACAGGATGAGGACACCTGACTCTCTTAAGGAGCTGAGAGCCCAA 1860
Db |||||
QY 1690 CAACTAGCAGATACAGGATGAGGACACCTGACTCTCTTAAGGAGCTGAGAGCCCAA 1749
Db |||||
QY 1861 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGTTACAGCAATGCTGCCCCATT 1920
Db |||||
QY 1750 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGTTACAGCAATGCTGCCCCATT 1809
Db |||||
QY 1921 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1980
Db |||||
QY 1810 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1869
Db |||||
QY 1981 AATATCTCTGTTAATATGTTGATACATTTCTTCTGATATTTTCTACATACATGATA 2040
Db |||||
QY 1870 AATATCTCTGTTAATATGTTGATACATTTCTTCTGATATTTTCTACATACATGATA 1929
Db |||||
QY 2041 AATATCTCTTCTTTTAAATAGGTTGATCTATGCTTTATGATGCTTTTATGAT 2100
Db |||||
QY 1930 AATATCTCTTCTTTTAAATAGGTTGATCTATGCTTTTATGATGCTTTTATGAT 1989
Db |||||
QY 2101 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAGCAAGCAAAAAAATTTTTAAAAA 2160
Db |||||
QY 1990 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAGCAAGCAAAAAAATTTTTAAAAA 2049
Db |||||
QY 2161 AAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAA 2220
Db |||||
QY 2050 AAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAA 2109
Db |||||
QY 2221 AAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAAATTTTTAAAAA 2261
Db |||||

Db |||||
2110 AA 2150
RESULT 10
ADS19439
ID ADS19439 standard; DNA; 2150 BP.
XX
AC ADS19439;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human secreted protein related to CD8 alpha chain DNA.
XX
KW human; gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 120..716
FT /*tag= a
FT /product= "CD8 alpha chain related protein"
XX
PN WO2004083404-A2.
XX
PD 30-SEP-2004.
XX
PF 19-MAR-2004; 2004WO-US008567.
XX
PR 19-MAR-2003; 2003US-0456378P.
XX
PA (ISOG-) ISOGENIS INC.
XX
PI Qi Y, Zhang X, Konigsberg PJ;
XX
WPI: 2004-691049/67.
P-PSDB; ADS19438.
XX
New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain operably linked to a nucleic acid encoding a transmembrane polypeptide, useful for inhibiting cellular and humoral components of the host immune responses.
XX
PS Disclosure; Fig 1; 94pp; English.
XX
This invention relates to novel gene therapy vectors with reduced immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8 alpha chain operably linked to nucleic acid encoding a transmembrane polypeptide and a second nucleic acid representing the therapeutic gene of interest (for example ornithine carbamoyl transferase or beta glucosidase), whereby transcriptional and translational control elements direct expression thereof. The present invention describes a method to reduce an immune response against antigens derived from a gene therapy delivery system i.e. improving the expression of a therapeutic transgene in a host and improving viral expression vectors with reduced immunogenicity. Accordingly, these compositions are useful for inhibiting both the cellular and humoral components of the host immune responses against expression vectors and target cells transfected with the vectors. As such, they exhibit immunosuppressive activity. This polynucleotide is the DNA sequence of a human secreted protein (derived from an alternate transcript) related to the CD8 alpha chain of the invention.
XX
SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;
Query Match 89.7%; Score 2029; DB 13; Length 2150;
Best Local Similarity 95.1%; Pred. No. 6.5e-276;
Matches 2150; Conservative 0; Mismatches 0; Indels 11; Gaps 1;
QY 1 GAAATCAGGCTCCGGGCCGGCGGAGGCGCAACTTTCCCTCCCTCGGCGCCACCGGCT 60
Db |||||
1 GAAATCAGGCTCCGGGCCGGCGGAGGCGCAACTTTCCCTCCCTCGGCGCCACCGGCT 60
Db |||||

QY 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCAAGACGCTCTGGGGAGCGCTCA 120
Db 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCAAGACGCTCTGGGGAGCGCTCA 120
QY 121 TGGCTTTACAGTGAACCGCTTGTCTCTGCGCGCTGGCGCTTGTCTCCACGCGCGCAGGC 180
Db 121 TGGCTTTACAGTGAACCGCTTGTCTCTGCGCGCTGGCGCTTGTCTCCACGCGCGCAGGC 180
QY 181 CGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
QY 241 TGAAGTGCACAGTGTCTGTCTCCAAACCGAGCTCGGCTGCTGTGCTCTTCCAGCCGC 300
Db 241 TGAAGTGCACAGTGTCTGTCTCCAAACCGAGCTCGGCTGCTGTGCTCTTCCAGCCGC 300
QY 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 360
Db 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 360
QY 361 CGAGGGGTGAGACACCCAGCGTTCTCGGCGAAGAGTTGGGGGACACCTTCTGCTCTCA 420
Db 361 CGAGGGGTGAGACACCCAGCGTTCTCGGCGAAGAGTTGGGGGACACCTTCTGCTCTCA 420
QY 421 CCTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTTCTCTCGGCCCTGAGCAACT 480
Db 421 CCTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTTCTCTCGGCCCTGAGCAACT 480
QY 481 CCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCGAAGCCCAACGACGC 540
Db 481 CCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCGAAGCCCAACGACGC 540
QY 541 CAGCGCGCGGACCAACCAACCGCGCCCAACCATCGCTGCGAGCCCTGTCTCGGCC 600
Db 541 CAGCGCGCGGACCAACCAACCGCGCCCAACCATCGCTGCGAGCCCTGTCTCGGCC 600
QY 601 CAGAGCGTCCGCGCAGCGCGGGGGGCGAGTGCACAGAGGGGCTGGACTTCGCGCT 660
Db 601 CAGAGCGTCCGCGCAGCGCGGGGGGCGAG----- 633
QY 661 GTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCCTGCTACTGG 720
Db 634 ----- 633
QY 721 TTATCACCTTTACTGCAACCAAGGAACCGAGAGCTGTGTTGCAAAATGTCCCGCGCTG 780
Db 634 -----GGAACCGAAGACGTGTGTTGCAATGTCCCGCGCTG 669
QY 781 TGGTCAATCGGAGACAAGCCAGCGCTTTCGCGAGATACGCTTAAACCTGTGCAACAG 840
Db 670 TGGTCAAAATCGGAGACAAGCCAGCGCTTTCGCGAGATACGCTTAAACCTGTGCAACAG 729
QY 841 CCACTACATTTACTTCAAACTGAGATCCTTCTTTGAGGAGCGAGTCTTCCCTTTCTAT 900
Db 730 CCACTACATTTACTTCAAACTGAGATCCTTCTTTGAGGAGCGAGTCTTCCCTTTCTAT 789
QY 901 TTTTTCAGTCTTCTCCCTGTGTATTCTATGATTATTTATTTAGTGGGGCGGG 960
Db 790 TTTTTCAGTCTTCTCCCTGTGTATTCTATGATTATTTATTTAGTGGGGCGGG 849
QY 961 GTGGGGAAGATTACTTTTTTTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTTAC 1020
Db 850 GTGGGGAAGATTACTTTTTTTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTTAC 909
QY 1021 AGTACACCAAGAGGTCAAACTACTTGTCTGCGCACATCGCGTAGGGGTGGAAAGGG 1080
Db 910 AGTACACCAAGAGGTCAAACTACTTGTCTGCGCACATCGCGTAGGGGTGGAAAGGG 969
QY 1081 CAGGGCCAGAGCTACCGCAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGCACCCATG 1140
Db 970 CAGGGCCAGAGCTACCGCAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGCACCCATG 1029
QY 1141 CCATCTCAACCTCTTCCCGCGCGCTTTTACAAAGGGGGAGGCTAAAGCCGACGAGACAGCT 1200

Db 1030 CCATCTCAACCTCTTCCCGCGCGTTTACAAAGGGGAGGCTAAAGCCGACGACAGCT 1089
QY 1201 TGAATCAAAAGCCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1260
Db 1090 TGAATCAAAAGCCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1149
QY 1261 GCTCAGGGCTCTTTCTCCACACCAATTCAGGTCTTTTCCGAGGGCCCTGTCTCAGGG 1320
Db 1150 GCTCAGGGCTCTTTCTCCACACCAATTCAGGTCTTTTCCGAGGGCCCTGTCTCAGGG 1209
QY 1321 TGAAGTGTGAGTCTCCAAACGGCAAGGAAACAGTACTTCTTGTATACCTTGGGATCTGT 1380
Db 1210 TGAAGTGTGAGTCTCCAAACGGCAAGGAAACAGTACTTCTTGTATACCTTGGGATCTGT 1269
QY 1381 GCCCAGAGCCTCAGAGAGTAATGAATTAAGAGAGAGTAAGTCTTTCGAGAGTTCTAT 1440
Db 1270 GCCCAGAGCCTCAGAGAGTAATGAATTAAGAGAGAGTAAGTCTTTCGAGAGTTCTAT 1329
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1500
Db 1330 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1389
QY 1501 AATAAATGAAGTGTGAGCTTAAACCTTGGAATGAATCCCTCTATCTCTAAAGAAAAAT 1560
Db 1390 AATAAATGAAGTGTGAGCTTAAACCTTGGAATGAATCCCTCTATCTCTAAAGAAAAAT 1449
QY 1561 CTCTGTAAACCCCTATGTGGAGCGGAATTCCTCCAGAGCCCTTGCATTCGAGAGGG 1620
Db 1450 CTCTGTAAACCCCTATGTGGAGCGGAATTCCTCCAGAGCCCTTGCATTCGAGAGGG 1509
QY 1621 CCCATGAAGAGAGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1680
Db 1510 CCCATGAAGAGAGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1569
QY 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTTGGGATCACTGATGA 1740
Db 1570 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTTGGGATCACTGATGA 1629
QY 1741 CTTTTTATACTTTGTAAGACAAATTTGAGAGCCCTCCACACAGCCCTGGCCTCTGCT 1800
Db 1630 CTTTTTATACTTTGTAAGACAAATTTGAGAGCCCTCCACACAGCCCTGGCCTCTGCT 1689
QY 1801 CAACTAGCAGATACAGGATGAGGACGCTGACTCTCTTTAAGAGGCTGAGAGCCCAAA 1860
Db 1690 CAACTAGCAGATACAGGATGAGGACGCTGACTCTCTTTAAGAGGCTGAGAGCCCAAA 1749
QY 1861 CTGCTGTCCAAACATGCACTTCTTGTCTTAAAGGTATGTTACAAAGCAATGCCTGCCAAT 1920
Db 1750 CTGCTGTCCAAACATGCACTTCTTGTCTTAAAGGTATGTTACAAAGCAATGCCTGCCAAT 1809
QY 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATTAATCTTCACTTAGG 1980
Db 1810 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATTAATCTTCACTTAGG 1869
QY 1981 AATAATCTCTCTTAATATGTTGATCATTTCTTCTGATTTATTTCTACACATACATGTA 2040
Db 1870 AATAATCTCTCTTAATATGTTGATCATTTCTTCTGATTTATTTCTACACATACATGTA 1929
QY 2041 AATAATCTCTCTTTTAAATPAGGTTGTACTATGCTTGTATGAGTGGCTTTTAAATGAAT 2100
Db 1930 AATAATCTCTCTTTTAAATPAGGTTGTACTATGCTTGTATGAGTGGCTTTTAAATGAAT 1989
QY 2101 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCAAAAAAAGAAAAAAGAAAAA 2160
Db 1990 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCAAAAAAAGAAAAAAGAAAAA 2049
QY 2161 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2220
Db 2050 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2109
QY 2221 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2261

Db 2110 AA 2150

RESULT 11

ID ADZ26403 standard; cDNA; 2150 BP.

XX ADZ26403;

DT 16-JUN-2005 (first entry)

XX Human CD8 cDNA.

XX cell culture; stem cell; CD8; ss; gene.

XX Homo sapiens.

XX W02005030999-A1.

XX 07-APR-2005.

XX 24-SEP-2004; 2004WO-US031524.

XX 25-SEP-2003; 2003US-0506221P.

PR 08-OCT-2003; 2003US-0509594P.

XX (DAND) DANA FARBER CANCER INST INC.

XX Ritz J, Wu CJ;

XX WPI; 2005-273394/28.

DR P-PSDB; ADZ26404.

XX Detecting lineage-specific cells in a biological sample, useful for
PT determining the clinical outcome of a progenitor cell transfer in a
PT subject, comprises identifying lineage-specific mRNA in the sample.

XX Disclosure; SEQ ID NO 29; 393pp; English.

XX The invention relates to a method of detecting lineage-specific cells in
CC a biological sample which comprises identifying lineage-specific mRNA in
CC the sample. The methods are useful for determining the clinical outcome
CC of a progenitor cell transfer in a subject, and for identifying or
CC quantifying lineage-specific cells. The present sequence represents a
CC human cDNA that encodes a protein used to identify lineage-specific
CC cells.

XX SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

Query Match 89.7%; Score 2029; DB 14; Length 2150;

Best Local Similarity 95.1%; Pred. No. 6.5e-276;

Matches 2150; Conservative 0; Mismatches 0; Indels 111; Gaps 1;

QY 1 GAAATCAGGCTCCGGCGCGCGCGAAGGGGCGCAACTTCCCCCTCGGCGCGCCACCGGCT 60

Db 1 GAAATCAGGCTCCGGCGCGCGCGAAGGGGCGCAACTTCCCCCTCGGCGCGCCACCGGCT 60

QY 61 CCCGCGCGCTCCCTCGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 120

Db 61 CCCGCGCGCTCCCTCGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 120

QY 121 TGGCCTTACCAAGTACCGGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGGC 180

Db 121 TGGCCTTACCAAGTACCGGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGGC 180

QY 181 CGAGCCAGTTCGGGTGTCCGCTGGATCGGACCTGGAACTGGCGGAGCAGTGGAGC 240

Db 181 CGAGCCAGTTCGGGTGTCCGCTGGATCGGACCTGGAACTGGCGGAGCAGTGGAGC 240

QY 241 TGAAGTGCCAGGTGTGCTGTCCAAACCCGACGTCGGGCTGTCTGTGGCTTCTCCAGCCGC 300

Db 241 TGAAGTGCCAGGTGTGCTGTCCAAACCCGACGTCGGGCTGTCTGTGGCTTCTCCAGCCGC 300

QY 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGG 360

Db 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGG 360

QY 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCCTCA 420

Db 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCCTCA 420

QY 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480

Db 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480

QY 481 CCATCATGTACTTCCAGCCACTTCCGCGGCTCTTCTGCGCAAGAGCCCAACGACGC 540

Db 481 CCATCATGTACTTCCAGCCACTTCCGCGGCTCTTCTGCGCAAGAGCCCAACGACGC 540

QY 541 CAGCGCGCGACCAACCAACCGCGCGCCACCATCGCGTGCAGGCCCTGCTCGGCC 600

Db 541 CAGCGCGCGACCAACCAACCGCGCGCCACCATCGCGTGCAGGCCCTGCTCGGCC 600

QY 601 CAGAGGCGTCCGCGCGAGCGCGGGGCGGAGTGACACAGAGGGGCTGACTTCGCCT 660

Db 601 CAGAGGCGTCCGCGCGAGCGCGGGGCGGAGTGACACAGAGGGGCTGACTTCGCCT 660

QY 661 GTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTCACTGG 720

Db 661 GTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTCACTGG 720

QY 721 TTATCAGCCTTTACTGCAACCAACAGGAACCGAAGACGTGTTTGAATAATGTCCTCGGCCCTG 780

Db 721 TTATCAGCCTTTACTGCAACCAACAGGAACCGAAGACGTGTTTGAATAATGTCCTCGGCCCTG 780

QY 781 TGGTCAAATCGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG 840

Db 781 TGGTCAAATCGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG 840

QY 841 CCATCATATTAATCAAACTGAGATCCTTCTTGTGGGAGCAAGTCTTCCCTTTCAT 900

Db 841 CCATCATATTAATCAAACTGAGATCCTTCTTGTGGGAGCAAGTCTTCCCTTTCAT 900

QY 901 TTTTTCAGTCTTCTCTCTCTGTATTCATTTCTCATGATTAATTTTAGTGGGCGCGG 960

Db 901 TTTTTCAGTCTTCTCTCTCTGTATTCATTTCTCATGATTAATTTTAGTGGGCGCGG 960

QY 961 GTGGAAAGATTAATTTTCTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTAC 1020

Db 961 GTGGAAAGATTAATTTTCTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTAC 1020

QY 1021 AGTACACCAAGGGTCAATATCTGTTGCGGCACATCGCGTAGGCGTGAAGGGG 1080

Db 1021 AGTACACCAAGGGTCAATATCTGTTGCGGCACATCGCGTAGGCGTGAAGGGG 1080

QY 1081 CAGGCCAGAGTACCCCGCAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCCACCCATG 1140

Db 1081 CAGGCCAGAGTACCCCGCAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCCACCCATG 1140

QY 1141 CCATCTCAACTTTCCTTCCCGCGGTTTACAAAGGGGAGGCTAAAGCCCAAGAGAGCT 1200

Db 1141 CCATCTCAACTTTCCTTCCCGCGGTTTACAAAGGGGAGGCTAAAGCCCAAGAGAGCT 1200

QY 1201 TGATCAAGGCGACACAGCAAGTTCAGGTTGGAGCAGTAGCTGGAGGAGCTTGTCTCCCA 1260

Db 1201 TGATCAAGGCGACACAGCAAGTTCAGGTTGGAGCAGTAGCTGGAGGAGCTTGTCTCCCA 1260

QY 1261 GCTCAGGCTCTTCTCTCCACCACTTTCAGGCTTCTTCTTCCGAGGCCCTCTGTCAGGG 1320

Db 1261 GCTCAGGCTCTTCTCTCCACCACTTTCAGGCTTCTTCTTCCGAGGCCCTCTGTCAGGG 1320

QY 1321 TGAGGTGCTGAGTCTCAACGGCAAGGAAACAAGTACTTCTTGTATACCTGGGATCTGT 1380

Db 1321 TGAGGTGCTGAGTCTCAACGGCAAGGAAACAAGTACTTCTTGTATACCTGGGATCTGT 1380

QY 1381 GCCCAGAGCCTCGAGGAGTAAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440

Db 1381 GCCCAGAGCCTCGAGGAGTAAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440

Db 1270 G C C C A G A G C C T C G A G G A G T A T G A A T T A A G A G A G A A C T G C C T T T G G C A G A G T T C T A T 1329
Qy 1441 A A T G T A A A C A A T A T C A G A C T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 1500
Db 1330 A A T G T A A A C A A T A T C A G A C T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 1389
Qy 1501 A A T A A A T G A A G T G T G A G C T T A A C C C T G G A A A T G A A T C C C T T A T C T A T C T T A A G A A A A T 1560
Db 1390 A A T A A A T G A A G T G T G A G C T T A A C C C T G G A A A T G A A T C C C T T A T C T T A A G A A A T 1449
Qy 1561 C T C T G T G A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1620
Db 1450 C T C T G T G A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1509
Qy 1621 C C C A T G A A A G A G A C A G G C T A C C C C T T T A C A A T A G A A T T T G A G C A T C A G T A G G T T A A A 1680
Db 1510 C C C A T G A A A G A G A C A G G C T A C C C C T T T A C A A T A G A A T T T G A G C A T C A G T A G G T T A A A 1569
Qy 1681 C T A A G C C C T T T G A A T C T C T G A A T T T G A T A C A A A C A T G T T C C T G G A T C A C T A T G A 1740
Db 1570 C T A A G C C C T T T G A A T C T C T G A A T T T G A T A C A A A C A T G T T C C T G G A T C A C T A T G A 1629
Qy 1741 C T T T T A T A C T T T G T A A G A C A A T T T T G A G A G C C C C T C A C A G C C C T G C C T T G C T 1800
Db 1630 C T T T T A T A C T T T G T A A G A C A A T T T T G A G A G C C C C T C A C A G C C C T G C C T T G C T 1689
Qy 1801 C A A C T A G A G A T A C A G G A T A G G C A G C T C A C T C T C T T A A G A G C C T G A G A G C C A A A 1860
Db 1690 C A A C T A G A G A T A C A G G A T A G G C A G C T C A C T C T C T T A A G A G C C T G A G A G C C A A A 1749
Qy 1861 C T G C T G T C C C A A C A T G C A C T T C T T G T T A A G T A T G T A C A A G C A A T G C C T G C C C A T T 1920
Db 1750 C T G C T G T C C C A A C A T G C A C T T C T T G C T T A A G T A T G T A C A A G C A A T G C C T G C C C A T T 1809
Qy 1921 G A G A G A A A A A C T T A A G T A G A T A G A A A T A A G A A C C A C T C A T A A T T C T T C A C C T T A G G 1980
Db 1810 G G A G A G A A A A C T T A A G T A G A T A G A A A T A A G A A C C A C T C A T A A T T C T C A C C T T A G G 1869
Qy 1981 A A T A T C T C C T G T A A T A T G G T G T A C A T T C T T C C T G A T T A T T T C T A C A C A T A C A T G T A A 2040
Db 1870 A A T A T C T C C T G T A A T A T G G T A C A T T C T T C C T G A T T A T T T C T A C A C A T A C A T G T A A 1929
Qy 2041 A A T A T G T C T T C T T T T T A A T A G G T T G T A C T A T G T A T G A T G G C T T T A A T A G A T 2100
Db 1930 A A T A T G T C T T C T T T T T A A T A G G T T G T A C T A T G C T G T A T G A T G G C T T T A A T A G A T 1989
Qy 2101 A A A C A T T T G T A C A T C C T T T A A T A G G T A A A C A G C A 2160
Db 1990 A A A C A T T T G T A C A T C C T T T T A A T G G T A A A C A G C A 2049
Qy 2161 A 2220
Db 2050 A 2109
Qy 2221 A 2261
Db 2110 A 2150

RESULT 12
AED96282
ID AED96282 standard; DNA; 3518 BP.
XX AC AED96282;
XX XX
DT 26-JAN-2006 (first entry)
XX XX
DE Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 439.
XX XX
KW Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;

KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
XX C-reactive protein pentraxin-related; CRP; Genetic marker; ds.
OS Homo sapiens.
XX
PN WO2005107364-A2.
XX 17-NOV-2005.
XX
XX 27-JAN-2005; 2005WO-IB002407.
XX
XX 27-JAN-2004; 2004US-0539128P.
PR 27-JAN-2004; 2004US-0539128P.
PR 22-OCT-2004; 2004US-0620874P.
PR 22-OCT-2004; 2004US-0621004P.
PR 25-OCT-2004; 2004US-0621053P.
PR 25-OCT-2004; 2004US-0621072P.
PR 26-OCT-2004; 2004US-0621663P.
PR 27-OCT-2004; 2004US-0622016P.
PR 27-OCT-2004; 2004US-0622017P.
PR 27-OCT-2004; 2004US-0622320P.
PR 17-NOV-2004; 2004US-0628101P.
PR 17-NOV-2004; 2004US-0628112P.
PR 17-NOV-2004; 2004US-0628133P.
PR 17-NOV-2004; 2004US-0628134P.
PR 17-NOV-2004; 2004US-0628144P.
PR 17-NOV-2004; 2004US-0628145P.
PR 17-NOV-2004; 2004US-0628156P.
PR 17-NOV-2004; 2004US-0628165P.
PR 17-NOV-2004; 2004US-0628179P.
PR 17-NOV-2004; 2004US-0628190P.
PR 17-NOV-2004; 2004US-0628231P.
PR 17-NOV-2004; 2004US-0628251P.
PR 26-NOV-2004; 2004US-0630559P.
PR 08-DEC-2004; 2004US-0634075P.
PR 27-JAN-2005; 2005US-00043806.
XX
XX (COMP-) COMPUGEN LTD.
XX (COHE/) COHEN Y.
PI Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocararu GS;
PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX WPI; 2005-810779/82.
XX
XX New polynucleotide, useful for diagnosing a CRP variant-detectable disease or for selecting therapy for a CRP variant-detectable disease, e.g., myocardial infarction, coronary artery disease.
XX Disclosure; SEQ ID NO 439; 1670pp; English.
XX
XX The invention relates to a new isolated polynucleotide. The polynucleotide is useful for diagnosing a CRP variant-detectable disease, for monitoring disease progression or treatment efficacy or relapse of a CRP variant-detectable disease or for selecting therapy for a CRP variant-detectable disease, e.g., myocardial infarction, coronary artery disease, non-fatal or fatal stroke, peripheral vascular disease, congestive heart failure or sudden cardiac death. The present sequence represents a human C-reactive protein, pentraxin-related (CRP) associated marker DNA.
XX
SQ Sequence 3518 BP; 766 A; 1056 C; 907 G; 789 T; 0 U; 0 Other;

Query Match 84.3%; Score 1905; DB 14; Length 3518;
Best Local Similarity 94.8%; Pred. No. 1.7e-258;
Matches 2026; Conservative 0; Mismatches 0; Indels 111; Gaps 1;
Qy 1 GAAATCAGCTCCGGGCGGGCGGCGAAGGGGCGCAACTTTCCTCCCTCGGCGCCACCGGCT 60
Db 1489 GAAATCAGCTCCGGGCGGGCGGCGAAGGGGCGCAACTTTCCTCCCTCGGCGCCACCGGCT 1548

QY 61 CCGGGGCTCCCTCGCGCGGAGCTTCAGCCAGCAGGCTCCTGGGAGCGCTCA 120
Db |||||
1549 CCGCGGCGCTCCCTCGCGCGGAGCTTCAGCCAGCAGGCTCCTGGGAGCGCTCA 1608
QY |||||
121 TGGCCTTACAGTGAACCGCTTGTCTCCGCGCTGCGCTGCTCTCCACGCCGCGAGGC 180
Db |||||
1609 TGGCCTTACAGTGAACCGCTTGTCTCCGCGCTGCGCTGCTCTCCACGCCGCGAGGC 1668
QY |||||
181 CGAGCCAGTTCGGGTGTCGCGCTGGATCGGAACCTGGGCGAGACAGTGGAGC 240
Db |||||
1669 CGAGCCAGTTCGGGTGTCGCGCTGGATCGGAACCTGGGCGAGACAGTGGAGC 1728
QY |||||
241 TGAAGTGCAGGTGCTGTCTCAACCGAGCGTGGGCTGCTCGTGGCTCTTCCAGCGGC 300
Db |||||
1729 TGAAGTGCAGGTGCTGTCTCAACCGAGCGTGGGCTGCTCGTGGCTCTTCCAGCGGC 1788
QY |||||
301 CGCGCGCGCGCGAGTCCCACTTCTCTCTATACCTCTCCCAAAACAGGCCAGGGCG 360
Db |||||
1789 GCGGGCGCGCGCGAGTCCCACTTCTCTCTATACCTCTCCCAAAACAGGCCAGGGCG 1848
QY |||||
361 CCGAGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGACACCTTCGTCCTCA 420
Db |||||
1849 CCGAGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGACACCTTCGTCCTCA 1908
QY |||||
421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGGCCCTGAGCAACT 480
Db |||||
1909 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGGCCCTGAGCAACT 1968
QY |||||
481 CCATCATGTACTTCAGCCACTTTCGTCGCGGCTCTCTCCAGCGAAGCCACACGAGCG 540
Db |||||
1969 CCATCATGTACTTCAGCCACTTTCGTCGCGGCTCTCTCCAGCGAAGCCACACGAGCG 2028
QY |||||
541 CAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCGCCCTGCTCCCTGGGCC 600
Db |||||
2029 CAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCGCCCTGCTCCCTGGGCC 2088
QY |||||
601 CAGAGCGGTGCGGCGACGCGGGGGGGCGGAGTGCAACAGAGGGGGTGACATTCGGCT 660
Db |||||
2089 CAGAGCGGTGCGGCGACGCGGGGGGGCGGAG----- 2121
QY |||||
661 GTGATATCTACATCATCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCACCTGG 720
Db |||||
2122 ----- 2121
QY |||||
721 TTATCACCCCTTTACTGCAACCAAGAAACCGAAGACGTGTTTGCAAAATGTCCCGGCGCTG 780
Db |||||
2122 -----GGAACCGAAGACGTGTTTGCAAAATGTCCCGGCGCTG 2157
QY |||||
781 TGGTCAAAATCGGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 840
Db |||||
2158 TGGTCAAAATCGGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 2217
QY |||||
841 CCATACATTAATCAAACTGAGATCCTTCTTTTGGGAGCAAGTCCCTCCCTTTTCAT 900
Db |||||
2218 CCATACATTAATCAAACTGAGATCCTTCTTTTGGGAGCAAGTCCCTCCCTTTTCAT 2277
QY |||||
901 TTTTTCAGTCTTCTCCCTGTGTATTCATCTCATGATTAATTTTGTAGTGGGGGGGG 960
Db |||||
2278 TTTTTCAGTCTTCTCCCTGTGTATTCATCTCATGATTAATTTTGTAGTGGGGGGGG 2337
QY |||||
961 GTGGAAAGATTAATTTTCTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTTAC 1020
Db |||||
2338 GTGGAAAGATTAATTTTCTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTTAC 2397
QY |||||
1021 AGTACACCAAGGGTCACAATCTGTTGCGCACATCGCGTAGGCGTGGAAAGGG 1080
Db |||||
2398 AGTACACCAAGGGTCACAATCTGTTGCGCACATCGCGTAGGCGTGGAAAGGG 2457
QY |||||
1081 CAGGCCAGAGCTACCCGAGAGTTCACAAATCATGCTGAGAGAGCTGGAGCACCCCATG 1140
Db |||||
2458 CAGGCCAGAGCTACCCGAGAGTTCACAAATCATGCTGAGAGAGCTGGAGCACCCCATG 2517
QY |||||
1141 CCATCTCAACCTTCTCCCGCGCGCTTTTACAAAGGGGGAGGCTAAAGCCAGAGACGCT 1200

Db |||||
2518 CCATCTCAACCTTCTCCCGCGCGCTTTTACAAAGGGGGAGGCTAAAGCCAGAGACGCT 2577
QY |||||
1201 TGATCAAAGGCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGGACCTTGTCTCCCA 1260
Db |||||
2578 TGATCAAAGGCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGGACCTTGTCTCCCA 2637
QY |||||
1261 GCTCAGGGCTCTTTCCTCCACACCATTCAGGTCTTCTTCCGAGGGCCCTGTCTCAGGG 1320
Db |||||
2638 GCTCAGGGCTCTTTCCTCCACACCATTCAGGTCTTCTTCCGAGGGCCCTGTCTCAGGG 2697
QY |||||
1321 TGAGGTCTTGAAGTCTCCACCGCAAGGGAACAAGTACTTCTTGATACCTGGGATACGT 1380
Db |||||
2698 TGAGGTCTTGAAGTCTCCACCGCAAGGGAACAAGTACTTCTTGATACCTGGGATACGT 2757
QY |||||
1381 GCCCAGAGCCTCGAGGAGTAAATGAATTAAGAAAGAGAACTGCCTTTGGCAGAGTCTAT 1440
Db |||||
2758 GCCCAGAGCCTCGAGGAGTAAATGAATTAAGAAAGAGAACTGCCTTTGGCAGAGTCTAT 2817
QY |||||
1441 AATGTAAACAATATCAGACTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 1500
Db |||||
2818 AATGTAAACAATATCAGACTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 2877
QY |||||
1501 AATAAATGAAGTGTGAGCTTAAACCTGGAAAATGAATCCTCTATCTCTAAAGAAAAT 1560
Db |||||
2878 AATAAATGAAGTGTGAGCTTAAACCTGGAAAATGAATCCTCTATCTCTAAAGAAAAT 2937
QY |||||
1561 CTCTGTGAAAACCCCTATGTGGAGCGGAAATGTCTCTCCAGCCCTTGATTCGAGAGGG 1620
Db |||||
2938 CTCTGTGAAAACCCCTATGTGGAGCGGAAATGTCTCTCCAGCCCTTGATTCGAGAGGG 2997
QY |||||
1621 CCCATGAAGAGGACAGGCTTACCCCTTTAACAATAGAAATTTGAGCATCAGTGAGTTAAA 1680
Db |||||
2998 CCCATGAAGAGGACAGGCTTACCCCTTTAACAATAGAAATTTGAGCATCAGTGAGTTAAA 3057
QY |||||
1681 CTAAGGCCCTCTTCAATCTCTGAATTTGAGATACAAACATGTCTCTGGGATCAGTGATGA 1740
Db |||||
3058 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTCTCTGGGATCAGTGATGA 3117
QY |||||
1741 CTTTATATCTTTGTAAGACAAATTTGGAGAGCCCTCTCACAGCCCTGGCCTCTGCT 1800
Db |||||
3118 CTTTATATCTTTGTAAGACAAATTTGGAGAGCCCTCTCACAGCCCTGGCCTCTGCT 3177
QY |||||
1801 CACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGAGGCTGAGAGCCCAA 1860
Db |||||
3178 CACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGAGGCTGAGAGCCCAA 3237
QY |||||
1861 CTGCTGTCCCAACATGCACTTCTCTTAAAGGTATGTTTAAAGCAATGCTGCCCAT 1920
Db |||||
3238 CTGCTGTCCCAACATGCACTTCTCTTAAAGGTATGTTTAAAGCAATGCTGCCCAT 3297
QY |||||
1921 GGAGAGAAAAAATTAAGTAGATAAGAAAATAAGAACCACTCATAAATTTCTCACCTTAGG 1980
Db |||||
3298 GGAGAGAAAAAATTAAGTAGATAAGAAAATAAGAACCACTCATAAATTTCTCACCTTAGG 3357
QY |||||
1981 AATAATCTCTGTTAAATAGGTGATACATCTCTCTGATATTTTCTACACATACATGATA 2040
Db |||||
3358 AATAATCTCTGTTAAATAGGTGATACATCTCTCTGATATTTTCTACACATACATGATA 3417
QY |||||
2041 AATAATCTCTTCTTTTAAATAGGTGATGCTGTTTATGATGCTGCTTTTAAATGAAT 2100
Db |||||
3418 AATAATCTCTTCTTTTAAATAGGTGATGCTGTTTATGATGCTGCTTTTAAATGAAT 3477
QY |||||
2101 AAACATTTGTAGCATCTCTTTTAAATGGGTAACAGCA 2137
Db |||||
3478 AAACATTTGTAGCATCTCTTTTAAATGGGTAACAGCA 3514

RESULT 13
AED96284
ID AED96284 standard; DNA; 3476 BP.
XX
AC AED96284;

XX 26-JAN-2006 (first entry)
XX Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 441.
DE Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
XX C-reactive protein pentraxin-related; CRP; genetic marker; ds.
OS Homo sapiens.
XX WO2005107364-A2.
XX 17-NOV-2005.
XX 27-JAN-2005; 2005WO-IB002407.
XX 27-JAN-2004; 2004US-0539128P.
PR 27-JAN-2004; 2004US-0539129P.
PR 22-OCT-2004; 2004US-0620874P.
PR 22-OCT-2004; 2004US-0621004P.
PR 25-OCT-2004; 2004US-0621053P.
PR 25-OCT-2004; 2004US-0621072P.
PR 26-OCT-2004; 2004US-0621663P.
PR 27-OCT-2004; 2004US-0622016P.
PR 27-OCT-2004; 2004US-0622017P.
PR 27-OCT-2004; 2004US-0622320P.
PR 17-NOV-2004; 2004US-0628101P.
PR 17-NOV-2004; 2004US-0628112P.
PR 17-NOV-2004; 2004US-0628133P.
PR 17-NOV-2004; 2004US-0628134P.
PR 17-NOV-2004; 2004US-0628144P.
PR 17-NOV-2004; 2004US-0628145P.
PR 17-NOV-2004; 2004US-0628156P.
PR 17-NOV-2004; 2004US-0628165P.
PR 17-NOV-2004; 2004US-0628179P.
PR 17-NOV-2004; 2004US-0628190P.
PR 17-NOV-2004; 2004US-0628231P.
PR 17-NOV-2004; 2004US-0628251P.
PR 26-NOV-2004; 2004US-0630559P.
PR 08-DEC-2004; 2004US-0634075P.
PR 27-JAN-2005; 2005US-00043806.
XX (COMP-) COMPUGEN LTD.
PA (COHE/) COHEN Y.
XX Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocaru GS;
PI Diber A, Novik A, Dahary D, Akiya P, Sorek R, Shemesh R;
XX WPI; 2005-810779/82.
XX New polynucleotide, useful for diagnosing a CRP variant-detectable
PT disease or for selecting therapy for a CRP variant-detectable
PT e.g., myocardial infarction, coronary artery disease.
XX Disclosure; SEQ ID NO 441; 1670pp; English.
XX The invention relates to a new isolated polynucleotide. The
CC polynucleotide is useful for diagnosing a CRP variant-detectable disease,
CC for monitoring disease progression or treatment efficacy or relapse of a
CC CRP variant-detectable disease or for selecting therapy for a CRP variant
CC -detectable disease, e.g., myocardial infarction, coronary artery
CC disease, non-fatal or fatal stroke, peripheral vascular disease,
CC congestive heart failure or sudden cardiac death. The present sequence
CC represents a human C-reactive protein, pentraxin-related (CRP) associated
CC marker DNA.
XX Sequence 3476 BP; 760 A; 1026 C; 886 G; 804 T; 0 U; 0 Other;
SQ

Query Match 80.5%; Score 1821; DB 14; Length 3476;
Best Local Similarity 92.8%; Pred. No. 1e-246; 0; Mismatches 153; Gaps 1;
Matches 1984; Conservative 0;
QY 1 GAAATCAGGCTCGGGCCGGCCGAGGGCGCAACTTTCCCTCCCTCGGGCCGCCACCGGCT 60
DB 1489 GAAATCAGGCTCGGGCCGGCCGAGGGCGCAACTTTCCCTCCCTCGGGCCGCCACCGGCT 1548
QY 61 CCGGCGCGCTCCCTCGGGCCGGCCGAGCTTCGAGCCCAAGCAGCGTCTCTGGGAGCGGTCA 120
DB 1549 CCGGCGCGCTCCCTCGGGCCGGCCGAGCTTCGAGCCCAAGCAGCGTCTCTGGGAGCGGTCA 1608
QY 121 TGGCCCTTACCAGTGACCGCTTCTCTCGCGGTGCTGCTGCTCCACCGCCGAGGC 180
DB 1609 TGGCCCTTACCAGTGACCGCTTCTCTCGCGGTGCTGCTGCTCCACCGCCGAGGC 1668
QY 181 CGAGCCAGTTCGGGTGTCGGCTGGATCGAACCTGGGCGAGACAGTGAGC 240
DB 1669 CGAGCCAGTTCGGGTGTCGGCTGGATCGAACCTGGGCGAGACAGTGAGC 1728
QY 241 TGAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGTGCTGCTGGCTCTTCCAGCCGC 300
DB 1729 TGAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGTGCTGCTGGCTCTTCCAGCCGC 1788
QY 301 GCGGCGCGCCCGCAGTCCACCTTCTCTATACTCTCCCAAAACAAGCCCAAGCGCG 360
DB 1789 GCGGCGCGCCCGCAGTCCACCTTCTCTATACTCTCCCAAAACAAGCCCAAGCGCG 1848
QY 361 CGAGGGGCTGACACACCCAGCGGTCTCGGGCAAGAGTTCGGGACACCTTCGTCTCA 420
DB 1849 CCGAGGGGCTGACACACCCAGCGGTCTCGGGCAAGAGTTCGGGACACCTTCGTCTCA 1908
QY 421 CCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCTCGGCGCTTGAGCAACT 480
DB 1909 CCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCTCGGCGCTTGAGCAACT 1968
QY 481 CCATCATGTACTTCAGCCACTTCGTGCGCGGTCTTCTGCGCAGGAGCCACCCAGCAGC 540
DB 1969 CCATCATGTACTTCAGCC----- 1986
QY 541 GAGCGCGGGACCAACAACCGGGCGCCACCATCGCTCGAGCCCTTGTCTCTCGGC 600
DB 1987 ----- 1986
QY 601 CAGAGGCGTGGCGGCGAGCGGGCGCAGTGCACAGAGGGGCTTGACTTCGCT 660
DB 1987 -----ACTTCGCT 1995
QY 661 GTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTTCTCTGCTCACTGG 720
DB 1996 GTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTTCTCTGCTCACTGG 2055
QY 721 TTATCACCCTTTACTTGCAACCAACAGAACCGTGTTCGAAAATGTCCTCCCGGCTG 780
DB 2056 TTATCACCCTTTACTTGCAACCAACAGAACCGTGTTCGAAAATGTCCTCCCGGCTG 2115
QY 781 TGGTCAAAATCGGAGACAAGCCAGCTTCGCGCAGATACCTCTAAACCTCTGCAACAG 840
DB 2116 TGGTCAAAATCGGAGACAAGCCAGCTTCGCGCAGATACCTCTAAACCTCTGCAACAG 2175
QY 841 CCATCATATTACTTCAAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCTCTTTCAT 900
DB 2176 CCATCATATTACTTCAAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCTCTTTCAT 2235
QY 901 TTTTTCAGTCTTCTCTGCTGATTCATTCCTCATGATATATATTTAGTGGGCGGG 960
DB 2236 TTTTTCAGTCTTCTCTGCTGATTCATTCCTCATGATATATTTAGTGGGCGGG 2295
QY 961 GTGGAAAAGATTACTTTTCTTTATGTTTGAACGGAAACAAACTAGTTAAATCTAC 1020
DB 2296 GTGGAAAAGATTACTTTTCTTTATGTTTGAACGGAAACAAACTAGTTAAATCTAC 2355
QY 1021 AGTACACCAAGGGGTCAAAATACATCTGTTGCGCACATCGCGTAGGGCGTGGAAAGGGG 1080

Db 2356 AGTACACCAAGGGTCAACAATCTGTGTGCGCACATCGCGGTAGGCGGTGGAAGGGG 2415
Qy 1081 CAGGCCAGAGCTACCCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCCATG 1140
Db 2416 CAGGCCAGAGCTACCCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCCATG 2475
Qy 1141 CCATCTCAACCTTTCGCCGCCGCTTTTACAAAGGGGGAGGCTAAAGCCCAAGACAGCT 1200
Db 2476 CCATCTCAACCTTTCGCCGCCGCTTTTACAAAGGGGGAGGCTAAAGCCCAAGACAGCT 2535
Qy 1201 TGATCAAGGCACACAGCAAGCTCAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
Db 2536 TGATCAAGGCACACAGCAAGCTCAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 2595
Qy 1261 GCTCAGGCTCTTTCCTCCACACATTCAGGCTCTTTCCTCGAGGCCCCCTGCTCAGGG 1320
Db 2596 GCTCAGGCTCTTTCCTCCACACATTCAGGCTCTTTCCTCGAGGCCCCCTGCTCAGGG 2655
Qy 1321 TGAGGTGCTTGAGTCTCCACGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGT 1380
Db 2656 TGAGGTGCTTGAGTCTCCACGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGT 2715
Qy 1381 GCCCAGAGCTCGAGGAGTAAATGAATTAAGAGAGAGACTGCCTTTGGCAGAGTTCTAT 1440
Db 2716 GCCCAGAGCTCGAGGAGTAAATGAATTAAGAGAGAGACTGCCTTTGGCAGAGTTCTAT 2775
Qy 1441 AATGTAACAATATCAGACTTTTTTTTTTATATCAAGCCTAAATTTGATAGACTTAA 1500
Db 2776 AATGTAACAATATCAGACTTTTTTTTTTATATCAAGCCTAAATTTGATAGACTTAA 2835
Qy 1501 AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 2836 AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 2895
Qy 1561 CTCTGTGAACCCCTATGTGAGGCGGAATTTGCTCTCCAGGCCCTGCAATTCGACAGGG 1620
Db 2896 CTCTGTGAACCCCTATGTGAGGCGGAATTTGCTCTCCAGGCCCTGCAATTCGACAGGG 2955
Qy 1621 CCCATGAAGAGGACAGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA 1680
Db 2956 CCCATGAAGAGGACAGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA 3015
Qy 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA 1740
Db 3016 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA 3075
Qy 1741 CTTTTTATCTTTGAAAGACAAATTTGAGAGGCCCTTCACAGCCCTGGCCTCTGCT 1800
Db 3076 CTTTTTATCTTTGAAAGACAAATTTGAGAGGCCCTTCACAGCCCTGGCCTCTGCT 3135
Qy 1801 CAACCTAGCAGATACAGGATGAGGAGACCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
Db 3136 CAACCTAGCAGATACAGGATGAGGAGACCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 3195
Qy 1861 CTGCTGTCCCAACATGCACTCTCTTGTCTTAAGGTATGGTACAAACAATGCTGCCCAT 1920
Db 3196 CTGCTGTCCCAACATGCACTCTCTTGTCTTAAGGTATGGTACAAACAATGCTGCCCAT 3255
Qy 1921 GGAGAGAAAAAATTAAGTAGATAGGAAATGAAGAACCACTCATATTTCTTCACCTTAGG 1980
Db 3256 GGAGAGAAAAAATTAAGTAGATAGGAAATGAAGAACCACTCATATTTCTTCACCTTAGG 3315
Qy 1981 AATAATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACACATACATGATA 2040
Db 3316 AATAATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACACATACATGATA 3375
Qy 2041 AATAATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACATGATGCTTTAATGAAT 2100
Db 3376 AATAATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACATGATGCTTTAATGAAT 3435
Qy 2101 AACAATTTGATGATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACATGATGCTTTAATGAAT 2137

Db 3436 AACAATTTGATGATCTCTTAAATAGGTGATACATTTCTCTGATTATTTCTACATGATGCTTTAATGAAT 3472
RESULT 14
AED96285
ID AED96285 standard; DNA; 3407 BP.
XX AED96285;
AC AED96285;
DT 26-JAN-2006 (first entry)
XX Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 442.
DE Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
KW C-reactive protein pentraxin-related; CRP; genetic marker; ds.
XX Homo sapiens.
XX WO2005107364-A2.
XX 17-NOV-2005.
XX 27-JAN-2005; 2005WO-IB002407.
XX 27-JAN-2004; 2004US-0539128P.
XX 27-JAN-2004; 2004US-0539129P.
XX 22-OCT-2004; 2004US-0620874P.
XX 22-OCT-2004; 2004US-0621004P.
XX 25-OCT-2004; 2004US-0621053P.
XX 25-OCT-2004; 2004US-0621072P.
XX 26-OCT-2004; 2004US-0621663P.
XX 27-OCT-2004; 2004US-0622016P.
XX 27-OCT-2004; 2004US-0622017P.
XX 27-OCT-2004; 2004US-0622320P.
XX 17-NOV-2004; 2004US-0628101P.
XX 17-NOV-2004; 2004US-0628112P.
XX 17-NOV-2004; 2004US-0628133P.
XX 17-NOV-2004; 2004US-0628134P.
XX 17-NOV-2004; 2004US-0628144P.
XX 17-NOV-2004; 2004US-0628145P.
XX 17-NOV-2004; 2004US-0628156P.
XX 17-NOV-2004; 2004US-0628165P.
XX 17-NOV-2004; 2004US-0628179P.
XX 17-NOV-2004; 2004US-0628190P.
XX 17-NOV-2004; 2004US-0628231P.
XX 17-NOV-2004; 2004US-0628251P.
XX 26-NOV-2004; 2004US-0630559P.
XX 08-DEC-2004; 2004US-0634075P.
XX 27-JAN-2005; 2005US-00043806.
XX (COMP-) COMPUGEN LTD.
PA (COHE/) COHEN Y.
XX Toporik A, Pollock S, Levine Z, Avalon-Soffer M, Cojocaru GS;
PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
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PT e.g., myocardial infarction, coronary artery disease.
XX Disclosure; SEQ ID NO 442; 1670pp; English.
PS The invention relates to a new isolated polynucleotide. The
XX polynucleotide is useful for diagnosing a CRP variant-detectable disease,
CC for monitoring disease progression or treatment efficacy or relapse of a
CC CRP variant-detectable disease or for selecting therapy for a CRP variant

CC -detectable disease, e.g., myocardial infarction, coronary artery
CC disease, non-fatal or fatal stroke, peripheral vascular disease,
CC congestive heart failure or sudden cardiac death. The present sequence
CC represents a human C-reactive protein, pentraxin-related (CRP) associated
XX marker DNA.

Sequence 3407 BP; 748 A; 1005 C; 871 G; 783 T; 0 U; 0 Other;

Query Match 74.4%; Score 1683; DB 14; Length 3407;
Best Local Similarity 89.6%; Pred. No. 2.4e-227;
Matches 1915; Conservative 0; Mismatches 0; Indels 222; Gaps 1;

QY 1 GAAATCAGGCTCGGCGCGCGCGAAGGGGCGCAACTTCCCGCTCGGCGCGCGCGCT 60
DB 1489 GAAATCAGGCTCGGCGCGCGCGAAGGGGCGCAACTTCCCGCTCGGCGCGCGCGCT 1548

QY 61 CCGCGCGCTCCCTCGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 120
DB 1549 CCGCGCGCTCCCTCGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 1608

QY 121 TGGCCCTTACAGTGACCGGCTTGCTCCTCGCGCTGGCTTGCTCCACGCGCGCGAGC 180
DB 1609 TGGCCCTTACAGTGACCGGCTTGCTCCTCGCGCTGGCTTGCTCCACGCGCGCGAGC 1668

QY 181 CGAGCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGGAGACAGTGGAGC 240
DB 1669 CGAGCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGGAGACAGTGGAGC 1728

QY 241 TGAAGTGCAGGTGCTGCTCCAAACCGACGCTCGGCTGCTGCTGCTTCCAGCGCG 300
DB 1729 TGAAGTGCAGGTGCTGCTCCAAACCGACGCTCGGCTGCTGCTGCTTCCAGCGCG 1788

QY 301 GGGGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGCG 360
DB 1789 GGGGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGCG 1848

QY 361 CGAGGGGTGACACCCAGCGGTTCTGGGCAAGAGTTGGGGAGACACTTGCCTCA 420
DB 1849 CGAGGGGTGACACCCAGCGGTTCTGGGCAAGAGTTGGGGAGACACTTGCCTCA 1908

QY 421 CCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTGCTCGGCGCTGAGCACT 480
DB 1909 CCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTGCTCGGCGCTGAGCACT 1968

QY 481 CCATCATGTACTTCAGCACTTCTGCGCGGTCTTCTGCGAGCGAAGCCCAACAGCG 540
DB 1969 CCATCATGTACTTCAGCACTTCTGCGCGGTCTTCTGCGAGCGAAGCCCAACAGCG 2010

QY 541 CAGCGCGCGACCAACACACCGGCGCCACCATCGCGTCGCGCGCTGTCCCTGCGCC 600
DB 2011 ----- 2010

QY 601 CAGAGCGTGGCGCGCGCGCGGGGGCGAGTGACACAGAGGGGGCTGGACTCGCCT 660
DB 2011 ----- 2010

QY 661 GTGATATCTACATCTGGGCGCGCTTGGCGGGACTTGTGGGGTCTCTCTCTGCTCACTGG 720
DB 2011 ----- 2010

QY 721 TTATCACCCCTTACTGCAACCAAGAGACGAGTGTGTGCAAAAGTCCCGGCGCTG 780
DB 2011 ----- 2010

QY 781 TGGTCAATCGGAGACAGCCAGCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG 840
DB 2047 TGGTCAATCGGAGACAGCCAGCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG 2106

QY 841 CCACCTACATTACTTCAAACTGAGATCTTCTCTTTTGGGGAGCAAGTCTCCCTTTTAT 900
DB 2107 CCACCTACATTACTTCAAACTGAGATCTTCTCTTTTGGGGAGCAAGTCTCCCTTTTAT 2166

QY 901 TTTTTCAGTCTTCTCCTGTGTATTTATCTCATGATTAATTAATTTAGTGGGGCGGG 960

DB 2167 TTTTTCAGTCTTCTCCTGTGTATTTATTTCTCATGATTAATTAATTTAGTGGGGCGGG 2226
QY 961 GTGGGAAAGATTACTTTTTTTTATGTGTTTACCGGAAACAAACTAGTAAATCTAC 1020
DB 2227 GTGGGAAAGATTACTTTTTTTTATGTGTTTACCGGAAACAAACTAGTAAATCTAC 2286
QY 1021 AGTACACCAAGGGGTCAATATCTGTTGGGCCATCGCGTAGGGGTGAAAGGGG 1080
DB 2287 AGTACACCAAGGGGTCAATATCTGTTGGGCCATCGCGTAGGGGTGAAAGGGG 2346
QY 1081 CAGGCCAGAGCTACCGCGAGGTTCTCAGAATCATGCTGAGAGAGCTGAGGACCCATG 1140
DB 2347 CAGGCCAGAGCTACCGCGAGGTTCTCAGAATCATGCTGAGAGAGCTGAGGACCCATG 2406
QY 1141 CCATCTCAACCTTCTCCCGCGCGTTTACAAAGGGGAGGCTAAAGCCACAGAGAGCT 1200
DB 2407 CCATCTCAACCTTCTCCCGCGCGTTTACAAAGGGGAGGCTAAAGCCACAGAGAGCT 2466
QY 1201 TGATCAAAAGGCACACAGCAAGTCAGGTTGGAGCAGTAGCTGGAGGAGCTTGTCTCCCA 1260
DB 2467 TGATCAAAAGGCACACAGCAAGTCAGGTTGGAGCAGTAGCTGGAGGAGCTTGTCTCCCA 2526
QY 1261 GCTCAGGGCTCTTCTCCTCACACCATTCAGGCTCTTTTCCGAGGCCCTGTCTCAGGG 1320
DB 2527 GCTCAGGGCTCTTCTCCTCACACCATTCAGGCTCTTTTCCGAGGCCCTGTCTCAGGG 2586
QY 1321 TGAGGTGCTTGAGTCTCCAAACCGGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 1380
DB 2587 TGAGGTGCTTGAGTCTCCAAACCGGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 2646
QY 1381 GCCCAGAGCCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCTTTGGCAGAGTTCTAT 1440
DB 2647 GCCCAGAGCCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCTTTGGCAGAGTTCTAT 2706
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCTTAAATTTGATAGACTAA 1500
DB 2707 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCTTAAATTTGATAGACTAA 2766
QY 1501 AATAAATGAAGTGTGAGCTTAAACCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
DB 2767 AATAAATGAAGTGTGAGCTTAAACCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 2826
QY 1561 CTCTGTGAAACCCCTTATGTGGAGGCGAATCTCTCCAGGCCCTTGCAATGCGAGGGG 1620
DB 2827 CTCTGTGAAACCCCTTATGTGGAGGCGAATCTCTCTCCAGGCCCTTGCAATGCGAGGGG 2886
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAATTTGAGCATCAGTGAGTTAAA 1680
DB 2887 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAATTTGAGCATCAGTGAGTTAAA 2946
QY 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 1740
DB 2947 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 3006
QY 1741 CTTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGCGCTCTGCT 1800
DB 3007 CTTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGCGCTCTGCT 3066
QY 1801 CAACTAGCAGATACAGGATGAGGACCTGAGCTCTCTTAAAGAGGCTGAGAGGCCAAA 1860
DB 3067 CAACTAGCAGATACAGGATGAGGACCTGAGCTCTCTTAAAGAGGCTGAGAGGCCAAA 3126
QY 1861 CTGCTGTCCCAACATGCACTTCTCTTGTGTAGGTATGGTACAGCAATGCTGCCATT 1920
DB 3127 CTGCTGTCCCAACATGCACTTCTCTTGTGTAGGTATGGTACAGCAATGCTGCCATT 3186
QY 1921 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTCACCTTAGG 1980
DB 3187 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTCACCTTAGG 3246
QY 1981 AATAATCTCCTGTTAATATGTTGATCACTTCTTCTGATTTATTTCTTACATACATGATA 2040

Db 3247 AATAATCTCTGTTAATAATGGTGACATCTTCTCTGATTATTTTCTACATACATGTAA 3306
Qy 2041 AATATGCTTTCTTTTAAATAGGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT 2100
Db 3307 AATATGCTTTCTTTTAAATAGGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT 3366
Qy 2101 AAACATTGTAGCATCTCTTTAATGGGTAACAGCA 2137
Db 3367 AAACATTGTAGCATCTCTTTAATGGGTAACAGCA 3403

RESULT 15

AE96281
ID AED96281 standard; DNA; 3743 BP.
XX AC AED96281;
XX XX
XX 26-JAN-2006 (first entry)
XX XX
XX Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 438.
XX DE
XX Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
XX KW Anti-rheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
XX KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
XX KW cerebrovascular disease; coronary artery disease;
XX KW cerebrovascular ischemia; peripheral vascular disease;
XX KW congestive heart failure; sudden cardiac death;
XX KW C-reactive protein pentraxin-related; CRP; genetic marker; ds.
XX XX
XX Homo sapiens.
XX XX
XX WO2005107364-A2.
XX XX
XX 17-NOV-2005.
XX XX
XX 27-JAN-2005; 2005WO-IB002407.
XX XX
XX 27-JAN-2004; 2004US-0539128P.
XX PR 27-JAN-2004; 2004US-0539129P.
XX PR 22-OCT-2004; 2004US-0620874P.
XX PR 22-OCT-2004; 2004US-0621004P.
XX PR 25-OCT-2004; 2004US-0621053P.
XX PR 25-OCT-2004; 2004US-0621072P.
XX PR 26-OCT-2004; 2004US-0621663P.
XX PR 27-OCT-2004; 2004US-0622016P.
XX PR 27-OCT-2004; 2004US-0622017P.
XX PR 27-OCT-2004; 2004US-0622320P.
XX PR 17-NOV-2004; 2004US-0628101P.
XX PR 17-NOV-2004; 2004US-0628112P.
XX PR 17-NOV-2004; 2004US-0628133P.
XX PR 17-NOV-2004; 2004US-0628134P.
XX PR 17-NOV-2004; 2004US-0628144P.
XX PR 17-NOV-2004; 2004US-0628145P.
XX PR 17-NOV-2004; 2004US-0628156P.
XX PR 17-NOV-2004; 2004US-0628165P.
XX PR 17-NOV-2004; 2004US-0628179P.
XX PR 17-NOV-2004; 2004US-0628190P.
XX PR 17-NOV-2004; 2004US-0628231P.
XX PR 17-NOV-2004; 2004US-0628251P.
XX PR 26-NOV-2004; 2004US-0630559P.
XX PR 08-DEC-2004; 2004US-0634075P.
XX PR 27-JAN-2005; 2005US-00043806.
XX XX
XX (COMP-) COMPUEN LTD.
XX PA (COHE/) COHEN Y.
XX XX
XX Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocaru GS;
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XX XX
XX WPI; 2005-810779/82.
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XX Disclosure; SEQ ID NO 438; 1670pp; English.
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CC disease, non-fatal or fatal stroke, peripheral vascular disease,
CC congestive heart failure or sudden cardiac death. The present sequence
CC represents a human C-reactive protein, pentraxin-related (CRP) associated
CC marker DNA.
XX
XX Sequence 3743 BP; 800 A; 1128 C; 960 G; 855 T; 0 U; 0 Other;
SQ
Query Match 74.4%; Score 1683; DB 14; Length 3743;
Best Local Similarity 89.6%; Pred. No. 2.4e-227;
Matches 1915; Conservative 0; Mismatches 0; Indels 222; Gaps 1;
Qy 1 GAAATCAGGCTCCGGGCGCGCGGCGCAAGGCGCAACTTTCCCTCGGCGCCCCACCGGT 60
Db 1825 GAAATCAGGCTCCGGGCGCGCGGCGCAAGGCGCAACTTTCCCTCGGCGCCCCACCGGT 1884
Qy 61 CCGCGCGCTCCCTCGGCGCGCGGCTTCAGCCAGCGGCTCCTGGGAGCGCGTCA 120
Db 1885 CCGCGCGCTCCCTCGGCGCGCGGCTTCAGCCAGCGGCTCCTGGGAGCGCGTCA 1944
Qy 121 TGGCTTTACCAAGTACCGGCTTGTCTCTCGCGCTGGGCTTGTCTCCACCGCGCCAGGC 180
Db 1945 TGGCTTTACCAAGTACCGGCTTGTCTCTCGCGCTGGGCTTGTCTCCACCGCGCCAGGC 2004
Qy 181 CGAGCCAGTTCGGGCTTCGCGCTGGATCGGAACCTGGAACTGGGCGAGACAGTGGAGC 240
Db 2005 CGAGCCAGTTCGGGCTTCGCGCTGGATCGGAACCTGGAACTGGGCGAGACAGTGGAGC 2064
Qy 241 TGAAGTGCAGGCTGCTGCTCCAAACCGAGTGGGCTGCTCGTGGCTTTCAGCCGC 300
Db 2065 TGAAGTGCAGGCTGCTGCTCCAAACCGAGTGGGCTGCTCGTGGCTTTCAGCCGC 2124
Qy 301 CGGCGCGCGCGCGAGTCCCACTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG 360
Db 2125 CGGCGCGCGCGCGAGTCCCACTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG 2184
Qy 361 CCGAGGGGCTGGACACCCAGCGGTTTCGGGCAAGAGTTGGGGAGACACTTCGTCCTCA 420
Db 2185 CCGAGGGGCTGGACACCCAGCGGTTTCGGGCAAGAGTTGGGGAGACACTTCGTCCTCA 2244
Qy 421 CCCTGAGCGACTTCGCGCGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCACT 480
Db 2245 CCCTGAGCGACTTCGCGCGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCACT 2304
Qy 481 CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCGGCTCTCTCCAG- 540
Db 2305 CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCGGCTCTCTCCAG- 2346
Qy 541 CAGCGCGCGACACCAACACACCGGCGCCACCATCGCGTGGAGCCCTGTCCCTCGCGCC 600
Db 2347 ----- 2346
Qy 601 CAGAGGCGTCCGGCGCGGCGGCGGCGGCGAGTGCACACAGGGGCTGGACTTCGCCT 660
Db 2347 ----- 2346
Qy 661 GTGATATCTACATCTGGGCGGCCCTTGGCGGGGACTTGTGGGCTCTTCTCTGTCACTGG 720
Db 2347 ----- 2346
Qy 721 TTATCACCCCTTTACTGCAACACAGGAACCGAGACGTTGTTGCAATGTTCCCGGCTG 780
Db 2347 -----GGAAACCGAGACGTTGTTGCAATGTTCCCGGCTG 2382
Qy 781 TGGTCAAAATCGGAGACAAAGCCAGCCTTTTCGGCGAGATACGCTCTAAACCTGTGCAACAG 840

||||| 2383 TGGTCAAAATCGGAGACAAGCCAGCCTTTCCGGCAGATACGCTCAACCCCTGTCACACAG 2442
QY CCACTACATTACTTTCAAACTGAGATCCTTCCCTTTTGGAGGAGCAAGTCCCTTCCCTTTTCAT 900
Db CCACTACATTACTTTCAAACTGAGATCCTTCCCTTTTGGAGGAGCAAGTCCCTTCCCTTTTCAT 2502
QY TTTTTCAGTCTTCCCTCCCTGTGTATTCATCTCATGATTAATTAATTTAGTGGGGCGGG 960
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Job time : 2544 secs

GenCore version 5.1.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2006, 11:06:58 ; Search time 721 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1048 | 46.4 | 1060 | 2 | US-07-940-605A-11 Sequence 11, Appl |
| 3 | 1048 | 46.4 | 1060 | 2 | US-08-690-096-11 Sequence 11, Appl |
| 4 | 1048 | 46.4 | 1060 | 3 | US-09-023-655-1014 Sequence 1014, Ap |
| 5 | 346.8 | 24.0 | 1131 | 3 | US-08-751-512-7 Sequence 7, Appl |
| 6 | 346.8 | 15.3 | 822 | 2 | US-08-403-853-11 Sequence 11, Appl |
| 7 | 193.8 | 8.6 | 803 | 3 | US-09-477-737-2 Sequence 2, Appl |
| 8 | 193.8 | 8.6 | 972 | 2 | US-07-940-605A-9 Sequence 9, Appl |
| 9 | 193.8 | 8.6 | 972 | 2 | US-08-690-096-9 Sequence 9, Appl |
| 10 | 133.6 | 5.9 | 240 | 2 | US-08-628-417-6 Sequence 6, Appl |
| 11 | 131.6 | 5.8 | 1459 | 3 | US-09-537-654-3 Sequence 3, Appl |
| 12 | 131.6 | 5.8 | 1459 | 5 | US-10-818-809-3 Sequence 3, Appl |
| 13 | 131.4 | 5.8 | 1798 | 3 | US-09-797-906-1 Sequence 1, Appl |
| 14 | 131 | 5.8 | 2394 | 3 | US-09-800-729-33 Sequence 33, Appl |
| 15 | 130.6 | 5.8 | 1696 | 3 | US-09-835-811-1 Sequence 1, Appl |
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| c 17 | 130.4 | 5.8 | 396 | 3 | US-09-640-173-53 Sequence 53, Appl |
| c 18 | 130.4 | 5.8 | 396 | 3 | US-09-713-550-53 Sequence 53, Appl |
| c 19 | 130.4 | 5.8 | 396 | 3 | US-09-825-294-53 Sequence 53, Appl |
| c 20 | 130.4 | 5.8 | 396 | 3 | US-09-970-966-53 Sequence 53, Appl |
| 21 | 130.4 | 5.8 | 2146 | 3 | US-10-003-392-3 Sequence 3, Appl |
| 22 | 130.4 | 5.8 | 2447 | 3 | US-09-014-969-14 Sequence 14, Appl |
| 23 | 129.6 | 5.7 | 3275 | 3 | US-09-370-838-151 Sequence 151, App |

ALIGNMENTS

RESULT 1
US-10-131-831-9109
; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Query Match 94.1%; Score 2127; DB 5; Length 2150;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Db 1 GGGTCATGGCCTTACCACTGACCGGCTTGTCTCGCGCTGGACCTGGACCTGGGCGGACAG 120
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Db 61 CCAGGCCGAGCCAGTTCCGGGTGTTCGGCTGGATCGGACCTGGAACTGGGCGGACAG 120
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Qy 415 TCCTCACCTGAGGACTTCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCCCTGA 474
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RESULT 2
US-07-940-605A-11
; Sequence 11, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-940-605A-11

Query Match 46.4%; Score 1048; DB 2; Length 1060;
Best Local Similarity 100.0%; Pred. No. 1.8e-217;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 607 CCGTCCGCGACGCGCGCGCGCGCGAGTGCACACGAGGGGGTGGACTTCGCTGTGATA 666
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QY 667 TCTACATCTGGCGCGCTTCGCGCGGACTGTGTGGGTCTTCTCTCTGTCACTGGTTATCA 726
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RESULT 3

US-08-690-096-11

; Sequence 11, Application US/08690096

; Patent No. 5945513

; GENERAL INFORMATION:

; APPLICANT: ARUFFO, ALEJANDRO

; APPLICANT: HOLLENBAUGH, DIANE

; APPLICANT: LEDBETTER, JEFFREY A.

; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: 31-JUL-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/940,605

; FILING DATE: 04-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Mirock, S. Lealie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 5624-184

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1060 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

| | | | |
|--------------------------------|------|--|------|
| ; MOLECULE TYPE: DNA (genomic) | | US-08-690-096-11 | |
| Query Match | | 46.4%; Score 1048; DB 2; Length 1060; | |
| Best Local Similarity | | 100.0%; Pred. No. 1.8e-217; | |
| Matches 1048; Conservative | | 0; Mismatches 0; Indels 0; Gaps 0; | |
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| Db | 13 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTGGGAGGCGGTCAATGCGCT | 72 |
| Qy | 127 | TACCAAGTACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCACAGGCGGAGCC | 186 |
| Db | 73 | TACCAAGTACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCACAGGCGGAGCC | 132 |
| Qy | 187 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAGACAGTGGAGCTGAAGT | 246 |
| Db | 133 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAGACAGTGGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGGTGCTGCTGCACCCGAGTGGGCTGCTGTGGCTCTTCCAGCGCGCGCG | 306 |
| Db | 193 | GCCAGGTGCTGCTGCACCCGAGTGGGCTGCTGTGGCTCTTCCAGCGCGCGCG | 252 |
| Qy | 307 | CCGCCCGCAGTCCACACTTCTCTATACCTCTCCCAAAACAAGCCAAAGCGCCGAGG | 366 |
| Db | 253 | CCGCCCGCAGTCCACACTTCTCTATACCTCTCCCAAAACAAGCCAAAGCGCCGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCTCAACCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCTCAACCTGA | 372 |
| Qy | 427 | GCGACTTCGCGGAGAGAACGAGGCTACTATTTCTGCTCGGCCCTGAGCAACTCCATCA | 486 |
| Db | 373 | GCGACTTCGCGGAGAGAACGAGGCTACTATTTCTGCTCGGCCCTGAGCAACTCCATCA | 432 |
| Qy | 487 | TGTACTTCAGCCACTTCGTGCGGCTTCTTCGCGAGGAGCCCAACGAGCGCCAGCGC | 546 |
| Db | 433 | TGTACTTCAGCCACTTCGTGCGGCTTCTTCGCGAGGAGCCCAACGAGCGCCAGCGC | 492 |
| Qy | 547 | CGCACCACCAACACCGCGCCGCCATCGCGTGGCGGCTGCTCCGCGCCAGAGG | 606 |
| Db | 493 | CGCACCACCAACACCGCGCCGCCATCGCGTGGCGGCTGCTCCGCGCCAGAGG | 552 |
| Qy | 607 | CGTGGCGCCAGCGCGCGCGCGCGAGTGACACAGAGGGGCTGACTTCGCTGTGATA | 666 |
| Db | 553 | CGTGGCGCCAGCGCGCGCGCGCGAGTGACACAGAGGGGCTGACTTCGCTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGCGCCCTTGGCGGAGCTTGTGGGCTCTTCTCTGCTCACTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGCGCCCTTGGCGGAGCTTGTGGGCTCTTCTCTGCTCACTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACACAGGAACCGAAGAGCTGTTTGCAAAATGTCCCGGCTGTGPTCA | 786 |
| Db | 673 | CCCTTTACTGCAACACAGGAACCGAAGAGCTGTTTGCAAAATGTCCCGGCTGTGPTCA | 732 |
| Qy | 787 | AATCGGAGACAAGCCAGCTTTCGCGAGATAGTCTTAACCTGTGTCACAGCCACTA | 846 |
| Db | 733 | AATCGGAGACAAGCCAGCTTTCGCGAGATAGTCTTAACCTGTGTCACAGCCACTA | 792 |
| Qy | 847 | CATTACTTCAAACTGAGATCTTCTCTTGGGAGCAAGTCTTCCCTTTTCATTTTTC | 906 |
| Db | 793 | CATTACTTCAAACTGAGATCTTCTCTTGGGAGCAAGTCTTCCCTTTTCATTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCCTGTGTATTCATTCTCATGATTAATTTTGTGGGGCGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCCTGTGTATTCATTCTCATGATTAATTTTGTGGGGCGGGTGGGA | 912 |
| Qy | 967 | AAGATTACTTTTCTTTATGTGTTTGACGGGAAACAAACTAGGTAAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTACTTTTCTTTATGTGTTTGACGGGAAACAAACTAGGTAAATCTACAGTACA | 972 |
| Qy | 1027 | CCACAAGGTCACAACTACTGTGTGCGCACATCGCGGTAGGCGGTGGAAAGGGCGGCC | 1086 |

US-09-023-655-1014

Query Match

Best Local Similarity

Matches 1048; Conservative

46.4%; Score 1048; DB 3; Length 1060;

100.0%; Pred. No. 1.8e-217;

0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|------|---|------|
| Db | 973 | CCACAAGGTCACAACTACTGTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGCGAGGCC | 1032 |
| Qy | 1087 | AGAGCTACCGCAGAGTTCTCAGAAATCA | 1114 |
| Db | 1033 | AGAGCTACCGCAGAGTTCTCAGAAATCA | 1060 |

RESULT 4

US-09-023-655-1014

Sequence 1014, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1014:

SEQUENCE CHARACTERISTICS:

LENGTH: 1060 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g179145

US-09-023-655-1014

Qy 67 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTGGGAGGCGGTCAATGCGCT | 126 || Db | 13 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTGGGAGGCGGTCAATGCGCT | 72 |
| Qy | 127 | TACCAAGTACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCACAGGCGGAGCC | 186 |
| Db | 73 | TACCAAGTACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCACAGGCGGAGCC | 132 |
| Qy | 187 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAGACAGTGGAGCTGAAGT | 246 |
| Db | 133 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAGACAGTGGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGGTGCTGCTGCACCCGAGTGGGCTGCTGTGGCTCTTCCAGCGCGCGCG | 306 |

Db 193 GCCAGGTGCTGTGTCACACCCGAGCTCGGGTGTCTGTGGCTTTCCAGCGCGCGGG 252
Qy 307 CGCGCGCCAGTCCCACTTCTCTTATACCTCTCCCAAAACAGCCCAAGCGCGCGAGG 366
Db 253 CGCGCGCCAGTCCCACTTCTCTTATACCTCTCCCAAAACAGCCCAAGCGCGCGAGG 312
Qy 367 GCGTGAACACCCAGCGGTTCTCGGGCAAGAGGTGGGGACACCTTGTCTCACCTGA 426
Db 313 GCGTGAACACCCAGCGGTTCTCGGGCAAGAGGTGGGGACACCTTGTCTCACCTGA 372
Qy 427 GCGACTTCGCGAGAGAGAGGCTACTATTCTGTCTCGGCTCGAGCACTCCATCA 486
Db 373 GCGACTTCGCGAGAGAGAGGCTACTATTCTGTCTCGGCTCGAGCACTCCATCA 432
Qy 487 TGTACTTCAGCCACTTCGTGCGGCTCTCTCGCGAGAGCCACACAGCCAGCGC 546
Db 433 TGTACTTCAGCCACTTCGTGCGGCTCTCTCGCGAGAGCCACACAGCCAGCGC 492
Qy 547 CGCGACCAACACACCGCGCCCAACATCGCTCGAGCCCTGTCTCGCGCCAGAGG 606
Db 493 CGCGACCAACACACCGCGCCCAACATCGCTCGAGCCCTGTCTCGCGCCAGAGG 552
Qy 607 CGTGCAGCGCGCGCGCGCGCGAGTGCACACGAGGGGCTGACTTCGCTGTGATA 666
Db 553 CGTGCAGCGCGCGCGCGCGCGAGTGCACACGAGGGGCTGACTTCGCTGTGATA 612
Qy 667 TCTACATCTGGCGGCTTGGCGGAGCTTGTGGGCTCTCTCTGTCTGCTGTTATCA 726
Db 613 TCTACATCTGGCGGCTTGGCGGAGCTTGTGGGCTCTCTCTGTCTGCTGTTATCA 672
Qy 727 CCCTTTACTGCAACACAGGAACCGAGAGCTGTTTGCAGATGTCTCCCGGCTGTGGTCA 786
Db 673 CCCTTTACTGCAACACAGGAACCGAGAGCTGTTTGCAGATGTCTCCCGGCTGTGGTCA 732
Qy 787 AATCGGAGACAAAGCCAGCCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCACTA 846
Db 733 AATCGGAGACAAAGCCAGCCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCACTA 792
Qy 847 CATTACTTCAAACTGAGATCTCTCTTTTGGGAGAGTCTCTTCCCTTTCATTTTTC 906
Db 793 CATTACTTCAAACTGAGATCTCTCTTTTGGGAGAGTCTCTTCCCTTTCATTTTTC 852
Qy 907 CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTATGTTGGGCGCGGTGGGA 966
Db 853 CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTATGTTGGGCGCGGTGGGA 912
Qy 967 AAGATTACTTTTCTTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTACAGTACA 1026
Db 913 AAGATTACTTTTCTTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTACAGTACA 972
Qy 1027 CCACAAGGTCAATATCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCAGGCC 1086
Db 973 CCACAAGGTCAATATCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCAGGCC 1032
Qy 1087 AGAGCTACCCGAGAGTTCTCAGAAATCA 1114
Db 1033 AGAGCTACCCGAGAGTTCTCAGAAATCA 1060

RESULT 5

us-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramey, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified PAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1128
us-08-751-512-7

Query Match 24.0%; Score 543; DB 3; Length 1131;
Best Local Similarity 100.0%; Pred. No. 5.9e-108;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 ATGGCTTTACAGTGACCGCTTGTCTGTGCGCTGGCTTGTCTGTCTCAACCGAGCTGGGAGACAGTGGAG 179
Db 1 ATGGCTTTACAGTGACCGCTTGTCTGTGCGCTGGCTTGTCTGTCTCAACCGAGCTGGGAGACAGTGGAG 60
Qy 180 CCGAGCCAGTTCGGGCTGTGCGCTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCGGGCTGTGCGCTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 120
Qy 240 CTGAAGTCCAGGTGCTGTCTGTCAACCGAGCTGGGCTGTCTGTCTTCCAGCGG 299
Db 121 CTGAAGTCCAGGTGCTGTCTGTCAACCGAGCTGGGCTGTCTGTCTTCCAGCGG 180
Qy 300 CGCGCGCGCGCGCGAGTCCCACTTCTCTTATACCTTCTCTCAAAACAAAGCCAGGCG 359
Db 181 CGCGCGCGCGCGCGAGTCCCACTTCTCTTATACCTTCTCTCAAAACAAAGCCAGGCG 240
Qy 360 GCGGAGGGCTGGACACCGAGGGTTCGCGGCAAGAGTTGGGGGACACCTTCTCTC 419
Db 241 GCGGAGGGCTGGACACCGAGGGTTCGCGGCAAGAGTTGGGGGACACCTTCTCTC 300
Qy 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTCGGCCCTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTCGGCCCTGAGCAAC 360
Qy 480 TCCATCATGTATTTTTCAGCCACTTGTGTGCGGCTTCTCTGCGGCAAGAGCTTCCCTGCGC 539
Db 361 TCCATCATGTATTTTTCAGCCACTTGTGTGCGGCTTCTCTGCGGCAAGAGCTTCCCTGCGC 420
Qy 540 CCAGCGCGCGCGCGCGAGCAACCGCGCGCCACCATCGGCTCGCAGCCCTGTCTCTGCGC 599
Db 421 CCAGCGCGCGCGCGAGCAACCGCGCGCCACCATCGGCTCGCAGCCCTGTCTCTGCGC 480
Qy 600 CCAGAGGGCTGCGCGCGAGCGCGGGGGCGGAGTGCACACGAGGGGGCTGACTTCGCC 659
Db 481 CCAGAGGGCTGCGCGCGAGCGCGGGGGCGGAGTGCACACGAGGGGGCTGACTTCGCC 540
Qy 660 TGT 662
|||


```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-690-096-9

Query Match      8.6%; Score 193.8; DB 2; Length 972;
Best Local Similarity 61.1%; Pred. No. 2.8e-32;
Matches 426; Conservative 0; Mismatches 247; Indels 24; Gaps 6;

Qy 185 CCAGTTCGGGTGTCGGGCTGGATCGGACCTGGGCGAGACAGTGGAGCTGAA 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 222 CGAACTCCGAATCTTCCAAAGAAATGGACGCCGAACCTTGGTCAGAGGTGGACCTGGT 281
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 245 GTGCCAGGTGCTGTGCCAACCGACGTGGGCTGCTCGTGGCTCTTCCAGCGCGCGG 304
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 282 ATGTGAAGTGTGGGTCCGGTTTCGCAAGGATGCTCTTGGCTCTTCCAGAACTCCAGCTC 341
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 CGCGCGCCGACAGTCCCACTTCTCTTATACCT-----CTCCCAAAACAGCCCAAGGC 358
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 342 CAAACTCCCCCAGCCACCTTCGTTGTATATATGCTTTCATCCCAACAAGATAACGTG 401
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 359 GGCCGAGGGGTGA---CACCAGCGGTTCGGGCGAAGG---TTGGGGACACCTT 412
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 402 GGACGAGAAGCTGAATTCGTGCAAACTGTTTCTGCCATGAGGACACGAATAAAGTA 461
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 413 CGTCTCACCCTGAGCACTTCCCGGAGAGAAAGAGGCTACTATTCTCTCGGCCCT 472
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 462 CGTTCTCACCCTGAGCACTTCCCGGAGAGAAAGAGGCTACTATTCTCTCAGTCAT 521
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 473 GAGCAACTCCATCATGTAATTCAGCCACTTCGTGCGCGGTCTTCTGCGAGCGAAGCCAC 532
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 522 CAGCAACTCGGTGATGTAATTCAGTTCTGTGTCAGTCTTCCAGAAAGTGAACCTCTAC 581
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 533 CACGAC---GCCAGCGCGGACACCAACAGCCGGCGCCACCATCGGTGCGAGCCCT 589
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 582 TACTACCAAGCCAGTGTGCGAATCCCTCCTACCTGTGCACCCCTACCGGGAC---ATCTCA 638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 590 GTCCCTCGCCGACAGGCGTCCGCGCAGCGCGGGGGCGCAGTCACACAGGGGGCT 649
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 639 GCGCCAGAGACAGAGATTGTCGGC-----CCGTTGGCTCAGTGAAGGGGACCGGATT 692
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 650 GGACTTCGCTGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCT 709
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 693 GGACTTCGCTGTGATATTTACATCTGGGCGCCCTTGGCGGGAACTCTGCGTGGCCCTCT 752
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 710 CCGTCACTGTTATACCCCTTTACTGCAACACAGGACCGAAGACGTGTTTGCATATG 769
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 753 GCTGTCTTGTATCATCTCTCATCTGTCTACACAGGAGCGGAAAGCGTGTGTCGAAATG 812
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 770 TCCCGCGCTGTGTCAAATCGGAGACAAACCGACGCTTTCGGCGGATACGCTCTAAC 829
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 813 TCCAGCGCGGTAGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 872
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 830 CTGTGCAACGCCACTACATTTACTTTCAACTGAGATC 866
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 873 TGGCAGCGCCAGGAAGCTACAACTACTACATGACTTC 909
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
```

ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (169)...(1011)
US-09-537-654-3

Query Match 5.8%; Score 131.6; DB 3; Length 1459;
Best Local Similarity 93.8%; Pred. No. 1e-18;
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2116 CCTCTTTAATGGTTAAACAGCAAAAAA 2175
Db 1294 CTCTCTGATCACCATGCAAAAAA 1353
Qy 2176 AAAAAA 2235
Db 1354 AAAAAA 1413
Qy 2236 AAAAAA 2261
Db 1414 AAAAAA 1439

RESULT 12
US-10-818-809-3
Sequence 3, Application US/10818809
Patent No. 7034117
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Shi, Jinrui
TITLE OF INVENTION: Rad51C Polypeptides and Uses Thereof
FILE REFERENCE: 1107D
CURRENT APPLICATION NUMBER: US/10/818,809
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: 60/132,582
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1459
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (169)...(1011)
US-10-818-809-3

Query Match 5.8%; Score 131.6; DB 5; Length 1459;
Best Local Similarity 93.8%; Pred. No. 1e-18;
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2116 CCTCTTTAATGGTTAAACAGCAAAAAA 2175
Db 1294 CTCTCTGATCACCATGCAAAAAA 1353
Qy 2176 AAAAAA 2235
Db 1354 AAAAAA 1413
Qy 2236 AAAAAA 2261
Db 1414 AAAAAA 1439

RESULT 13
US-09-797-906-1
Sequence 1, Application US/09797906
Patent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1798
TYPE: DNA
ORGANISM: Human
US-09-797-906-1

Query Match 5.8%; Score 131.4; DB 3; Length 1798;
Best Local Similarity 89.8%; Pred. No. 1.3e-18;
Matches 141; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 2105 ATTTCTAGCATCTCTTTAATGGTTAAACAGCAAAAAA 2164
Db 1620 ATTACAAACATGTCCTTGGCAGTGGAAAAA 1679
Qy 2165 AAAAAA 2224
Db 1680 AAAAAA 1739
Qy 2225 AAAAAA 2261
Db 1740 AAAAAA 1776

RESULT 14
US-09-800-729-33
Sequence 33, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 2394
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-33

Query Match 5.8%; Score 131; DB 3; Length 2394;
Best Local Similarity 96.4%; Pred. No. 1.8e-18;
Matches 134; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2123 AATGGTTAAACAGCAAAAAA 2182
Db 2249 AAAAGGAAAAAGGAAAAA 2308
Qy 2183 AAAAAA 2242
Db 2309 AAAAAA 2368
Qy 2243 AAAAAA 2261
Db 2369 AAAAAA 2387

RESULT 15
US-09-835-811-1
Sequence 1, Application US/09835811
Patent No. 6482936
GENERAL INFORMATION:
APPLICANT: HU, Song et al

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-835-811-1

Query Match 5.8%; Score 130.6; DB 3; Length 1696;
Best Local Similarity 93.8%; Pred. No. 1.8e-18;
Matches 136; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2117 CTCCTTTAATGGTTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2176
Db 1501 CACTGTATAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1560
Qy 2177 AA 2236
Db 1561 AA 1620
Qy 2237 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db 1621 AAAAAAAAAAAAAAAAAAAAAA 1645

Search completed: May 29, 2006, 12:38:41
Job time : 724 secs

Sequence 19, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 504, Appl
Sequence 503, Ap
Sequence 501, Ap
Sequence 5716, Ap
Sequence 5716, Ap
Sequence 5716, Ap
Sequence 5716, Ap
Sequence 5716, Ap
Sequence 5716, Ap
Sequence 6, Appl
Sequence 6, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 16232, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 6255, Ap
Sequence 6255, Ap
Sequence 6255, Ap
Sequence 6255, Ap
Sequence 6255, Ap
Sequence 24, Appl

ALIGNMENTS

1.1

; LIFE: DNA
; ORGANISM: Homo sapiens

| | Query Match | 100.0%; | Score 2261; | DB 9; | Length 2261; | |
|----|-----------------------|---|---------------|-----------|--------------|--|
| | Best Local Similarity | 100.0%; | Prod. No. 0; | | | |
| | Matches 2261; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 | |
| Qy | 1 | GAATCAGGCTCGGGCGCGCGAAGGGCGCAATTTTCCCCCTCGGGCCCCACCGGCT | 60 | | | |
| Db | 1 | GAATCAGGCTCGGGCGCGCGAAGGGCGCAATTTTCCCCCTCGGGCGCGCACCGGCT | 60 | | | |
| Qy | 61 | CCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAGCAGCTCTCGGGAGCGCGTCA | 120 | | | |
| Db | 61 | CCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAGCAGCTCTGGGGAGCGCTCA | 120 | | | |
| Qy | 121 | TGGCTTACAGTGACCGCTTGCTCTGCGCGCTTGGCTTGGCTGCTCCACGCCGACGCG | 180 | | | |
| Db | 121 | TGGCTTACAGTGACCGCTTGCTCTGCGCGCTTGGCTTGGCTGCTCCACGCCGACGCG | 180 | | | |
| Qy | 181 | CGAGCCAGTTCCGGGCTTCGCGCGCTGGATCGGACCTTGGAACTTGGGCGACAGCTGGAGC | 240 | | | |

Db 181 CGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAGC 240
Qy 241 TGAAGTCCAGGTGCTGTCTGTCGAACCCGAGCGTGGGCTGTCTGTGGCTCTTCCAGCGCG 300
Db 241 TGAAGTCCAGGTGCTGTCTGTCGAACCCGAGCGTGGGCTGTCTGTGGCTCTTCCAGCGCG 300
Qy 301 CGGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAACAGGCCCAAGGGGG 360
Db 301 CGGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAACAGGCCCAAGGGGG 360
Qy 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
Db 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
Qy 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Db 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Qy 481 CCATCATGTACTTCCAGCCACTTCTGCGGCTTCTTCTGCGGAGCGGCGGAGCGGCGGCGG 540
Db 481 CCATCATGTACTTCCAGCCACTTCTGCGGCTTCTTCTGCGGAGCGGCGGAGCGGCGGCGG 540
Qy 541 CAGCGCGGACACCAACACCGGCGGCCACCATCGGTCGCGAGCGGCTGTCCTGCGGCC 600
Db 541 CAGCGCGGACACCAACACCGGCGGCCACCATCGGTCGCGAGCGGCTGTCCTGCGGCC 600
Qy 601 CAGAGGGGTGCGGCGCAGCGGCGGGGCGCAGTGCACACGAGGGGGCTGACATTCGCGCT 660
Db 601 CAGAGGGGTGCGGCGCAGCGGCGGGGCGCAGTGCACACGAGGGGGCTGACATTCGCGCT 660
Qy 661 GTGATATCTACATCTGGGCGGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTGG 720
Db 661 GTGATATCTACATCTGGGCGGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTGG 720
Qy 721 TTATCACCCTTTACTGCAACACAGGAGAACGAGCGTGTGCAATGTCCCGGCGCTG 780
Db 721 TTATCACCCTTTACTGCAACACAGGAGAACGAGCGTGTGCAATGTCCCGGCGCTG 780
Qy 781 TGGTCAAACTCGGAGACAAAGCCAGCCTTTTCGGGAGATAGTCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAACTCGGAGACAAAGCCAGCCTTTTCGGGAGATAGTCTAAACCTGTGCAACAG 840
Qy 841 CCATCAATTAATCTAACTGAGATCTCTCTTTTGGGAGGAGCAAGTCTTCCCTTTTCA 900
Db 841 CCATCAATTAATCTAACTGAGATCTCTCTTTTGGGAGGAGCAAGTCTTCCCTTTTCA 900
Qy 901 TTTTTCAGTCTTCTCCCTGTGATTCATTTCTCATGATTAATTTTAGTGGGGGGGG 960
Db 901 TTTTTCAGTCTTCTCCCTGTGATTCATTTCTCATGATTAATTTTAGTGGGGGGGG 960
Qy 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTAC 1020
Db 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGAAGGAAACAAACTAGGTAAATCTAC 1020
Qy 1021 AGTACACACAAGGGTCAAAATCTGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGGG 1080
Db 1021 AGTACACACAAGGGTCAAAATCTGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGGG 1080
Qy 1081 CAGGCGAGGCTACCGCAGAGTTCTCAGATCATGCTGAGAGGCTGGAGGCCACCATG 1140
Db 1081 CAGGCGAGGCTACCGCAGAGTTCTCAGATCATGCTGAGAGGCTGGAGGCCACCATG 1140
Qy 1141 CCATCTCAACCTCTTCCCGCGCGGTTTTCAGAGGGGAGGCTAAAGCCCAAGAGACAGCT 1200
Db 1141 CCATCTCAACCTCTTCCCGCGCGGTTTTCAGAGGGGAGGCTAAAGCCCAAGAGACAGCT 1200
Qy 1201 TGATCAAAAGGCACACAGCAAGTCTAGGTTGAGCGAGTGGAGGACCTTGTCTCCA 1260
Db 1201 TGATCAAAAGGCACACAGCAAGTCTAGGTTGAGCGAGTGGAGGACCTTGTCTCCA 1260
Qy 1261 GCTCAGGCTCTTCTCCTCCACACCATTCAGGTCTTCTTCTTCCGAGGCGGCTGTCTCAGG 1320
Db 1261 GCTCAGGCTCTTCTCCTCCACACCATTCAGGTCTTCTTCTTCCGAGGCGGCTGTCTCAGG 1320

Qy 1321 TGAGGTCTTGAAGTCTCCAAACGCGCAAGGAAACAGTACTTCTTGATACCTCGGATACTGT 1380
Db 1321 TGAGGTCTTGAAGTCTCCAAACGCGCAAGGAAACAGTACTTCTTGATACCTCGGATACTGT 1380
Qy 1381 GCCCAGAGCCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCGCTTTGGCAGAGTTCTAT 1440
Db 1381 GCCCAGAGCCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCGCTTTGGCAGAGTTCTAT 1440
Qy 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCATAAATGTATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCATAAATGTATAGACCTAA 1500
Qy 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Qy 1561 CTCTGTAAACCCCTATGTGGAGCGGAAATGCTCTCCAGCCCTTGCAATTCAGAGGGG 1620
Db 1561 CTCTGTAAACCCCTATGTGGAGCGGAAATGCTCTCCAGCCCTTGCAATTCAGAGGGG 1620
Qy 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Qy 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGCGGATCACTGATGA 1740
Db 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGCGGATCACTGATGA 1740
Qy 1741 CTTTTTATACCTTTGAAGACAATTTGGAGAGCCCTCACAGCCCTGGCCTCTGCT 1800
Db 1741 CTTTTTATACCTTTGAAGACAATTTGGAGAGCCCTCACAGCCCTGGCCTCTGCT 1800
Qy 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Db 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Qy 1861 CTGCTGTCCCAACATGCACCTTCTTAAAGGTATGGTACAAAGCAATGCTGCCATTT 1920
Db 1861 CTGCTGTCCCAACATGCACCTTCTTAAAGGTATGGTACAAAGCAATGCTGCCATTT 1920
Qy 1921 GGAGAGAAACCTTAAGTAGATAGGAAATAGAACCACTCATATTTCTTCCACCTTAGG 1980
Db 1921 GGAGAGAAACCTTAAGTAGATAGGAAATAGAACCACTCATATTTCTTCCACCTTAGG 1980
Qy 1981 AATAATCTCTGTTAATATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
Qy 2041 AATAATCTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAT 2100
Db 2041 AATAATCTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAT 2100
Qy 2101 AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAACCAAAACCAAAACCAAA 2160
Db 2101 AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAACCAAAACCAAAACCAAA 2160
Qy 2161 AA 2220
Db 2161 AA 2220
Qy 2221 AA 2261
Db 2221 AA 2261

RESULT 2
US-10-888-313A-99
; Sequence 99, Application US/10888313A
; Publication No. US20050100934A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Kevin
; APPLICANT: AXEL, Richard

APPLICANT: STRAPPS, Walter
APPLICANT: BARNEA, Gilad
TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction
FILE REFERENCE: SENTI 203.2
CURRENT APPLICATION NUMBER: US/10/888,313A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/566,113
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60/511,918
PRIOR FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/485,968
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 99
LENGTH: 2261
TYPE: DNA
ORGANISM: homo sapiens
US-10-888-313A-99

Query Match 100.0%; Score 2261; DB 10; Length 2261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAGGCTCCGGCGCGCGCGAGGGCGCAACTTCCCTCGGCGCCCCACCGGCT 60
DB 1 GAAATCAGGCTCCGGCGCGCGCGAGGGCGCAACTTCCCTCGGCGCCCCACCGGCT 60

QY 61 CCCGCGCGCTCCCTCGGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGGAGCGGTCA 120
DB 61 CCCGCGCGCTCCCTCGGCGCGCGCGAGCTTCGAGCCAAAGCAGCGTCTCGGGGAGCGGTCA 120

QY 121 TGGCTTACAGTACCGCTTGTCTCTGCGCGCTTGTCTGCTCCAGCGCCGACGCG 180
DB 121 TGGCTTACAGTACCGCTTGTCTCTGCGCGCTTGTCTGCTCCAGCGCCGACGCG 180

QY 181 CGAGCGAGTTCGGGTGTCGCGCTGATCGACCTGAGACCTGGCGGAGACAGTGGAGC 240
DB 181 CGAGCGAGTTCGGGTGTCGCGCTGATCGACCTGAGACCTGGCGGAGACAGTGGAGC 240

QY 241 TGAAGTGCAGGTGTGCTGCTCCAAACCGGAGTTCGGGTGCTGCTGCTTCCAGCGCG 300
DB 241 TGAAGTGCAGGTGTGCTGCTCCAAACCGGAGTTCGGGTGCTGCTGCTTCCAGCGCG 300

QY 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGGCGG 360
DB 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGGCGG 360

QY 361 CCGAGGGCTGACACCCAGCGGTCTCGGGCAAGAGTTCGGGGACACCTTCGCTCTCA 420
DB 361 CCGAGGGCTGACACCCAGCGGTCTCGGGCAAGAGTTCGGGGACACCTTCGCTCTCA 420

QY 421 CCTGAGCGACTTCGCGGAGAGACGAGGGTACTATTCTGCTCGGCGCTGAGCAACT 480
DB 421 CCTGAGCGACTTCGCGGAGAGACGAGGGTACTATTCTGCTCGGCGCTGAGCAACT 480

QY 481 CCATCATGTACTTCAGCCACTTCGTCGCGGTCTTCTGCCAGCGAAGCCACGACGCG 540
DB 481 CCATCATGTACTTCAGCCACTTCGTCGCGGTCTTCTGCCAGCGAAGCCACGACGCG 540

QY 541 CAGCGCGGGACCAACACACCGCGCGCCACCATCGGTTCGAGCCCTGTCCTGCGCGC 600
DB 541 CAGCGCGGGACCAACACACCGCGCGCCACCATCGGTTCGAGCCCTGTCCTGCGCGC 600

QY 601 CAGGGCTGCGCGGAGCGGGGCGAGTGCACACGAGGGGCTGGACTTCGCT 660
DB 601 CAGGGCTGCGCGGAGCGGGGCGAGTGCACACGAGGGGCTGGACTTCGCT 660

QY 661 GTGATATCTACATCTGGGCGCGCTTGGCGGAGCTTGTGGGTCTTCTCTGTCACCTGG 720
DB 661 GTGATATCTACATCTGGGCGCGCTTGGCGGAGCTTGTGGGTCTTCTCTGTCACCTGG 720

QY 721 TTATCACCCTTTACTGCAACCAAGAGACCGAGAGACGTTTTCGCAAAATGTCCCGCGCTG 780
DB 721 TTATCACCCTTTACTGCAACCAAGAGACCGAGAGACGTTTTCGCAAAATGTCCCGCGCTG 780

DB 721 TTATCACCCTTTACTGCAACCAAGAGACCGAGAGACGTTTTCGCAAAATGTCCCGCGCTG 780
QY 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTTCGGCGAGATACGCTCTAAACCTGTGCAACAG 840
DB 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTTCGGCGAGATACGCTCTAAACCTGTGCAACAG 840
QY 841 CCATCATGTACTTCAAACTGAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTCAT 900
DB 841 CCATCATGTACTTCAAACTGAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTCAT 900
QY 901 TTTTTCAGTCTCTCTCCCTGATTCATCTCTCATGATTATTTATTTAGTGGGGCGG 960
DB 901 TTTTTCAGTCTCTCTCCCTGATTCATCTCTCATGATTATTTATTTAGTGGGGCGG 960
QY 961 GTGGAAAGATTACTTTTTTCTTTATGTGTGTTGACGGAAACAAACTAGTAAAACTCTAC 1020
DB 961 GTGGAAAGATTACTTTTTTCTTTATGTGTGTTGACGGAAACAAACTAGTAAAACTCTAC 1020
QY 1021 AGTACACCAAGGCTCAATACTGTTGTGCGCATCTCGCGTAGGGCGTGGAAAGGG 1080
DB 1021 AGTACACCAAGGCTCAATACTGTTGTGCGCATCTCGCGTAGGGCGTGGAAAGGG 1080
QY 1081 CAGGCGAGGCTACCCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCATG 1140
DB 1081 CAGGCGAGGCTACCCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCATG 1140
QY 1141 CCATCTCAACCTTCTCCCGCGCTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT 1200
DB 1141 CCATCTCAACCTTCTCCCGCGCTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT 1200
QY 1201 TGATCAAAAGGCAACAGCAAGTCAAGGTTGGAGAGTAGTACCTGGAGGACCTTGTCTCCA 1260
DB 1201 TGATCAAAAGGCAACAGCAAGTCAAGGTTGGAGAGTAGTACCTGGAGGACCTTGTCTCCA 1260
QY 1261 GCTCAGGCTCTTCTCCACACCACTCAGCTCTTCTTCCGAGGCGCTCTCTCAGGG 1320
DB 1261 GCTCAGGCTCTTCTCCACACCACTCAGCTCTTCTTCCGAGGCGCTCTCTCAGGG 1320
QY 1321 TGAGTGTCTTGAAGTCCAAAGGCAAGGAACTCTTCTGATACCTCGGATCTGT 1380
DB 1321 TGAGTGTCTTGAAGTCCAAAGGCAAGGAACTCTTCTGATACCTCGGATCTGT 1380
QY 1381 GCCAGAGCTTCGAGGAGGTAAATGAATTAAGAGAGAACTGCTTTCGAGAGTCTAT 1440
DB 1381 GCCAGAGCTTCGAGGAGGTAAATGAATTAAGAGAGAACTGCTTTCGAGAGTCTAT 1440
QY 1441 AATGTAAACATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGATAGACCTAA 1500
DB 1441 AATGTAAACATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGATAGACCTAA 1500
QY 1501 AATAAATGAAGTGTGAGCTTAAACCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
DB 1501 AATAAATGAAGTGTGAGCTTAAACCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
QY 1561 CTCTGTGAAACCCCTATGTGGAGCGGAAATGCTCTCCAGCCCTTGCAATTCAGAGGG 1620
DB 1561 CTCTGTGAAACCCCTATGTGGAGCGGAAATGCTCTCCAGCCCTTGCAATTCAGAGGG 1620
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTAAA 1680
DB 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTAAA 1680
QY 1681 CTAGGCGCTCTGAACTCTGAAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA 1740
DB 1681 CTAGGCGCTCTGAACTCTGAAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA 1740
QY 1741 CTTTATTACTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCACACAGCCCTGSCCTCTGCT 1800
DB 1741 CTTTATTACTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCACACAGCCCTGSCCTCTGCT 1800
QY 1801 CAATAGCAGATACAGGATGAGGACAGCTCTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
DB 1801 CAATAGCAGATACAGGATGAGGACAGCTCTCTCTTAAGGAGGCTGAGAGGCCAAA 1860

Db 1321 TGAGGTGCTGAGTCTCCAAACGGCAAGGAAACAAGTACTTCTTGATACCTGGGATACTGT 1380
Qy 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Db 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Qy 1441 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 1500
Qy 1501 AATAAAATGAAGTGTGAGCTTAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 1501 AATAAAATGAAGTGTGAGCTTAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Qy 1561 CTCTGTGAACCCCTATGTGGAGGCGAAATGCTCTCCAGCCCTTGCAATTCAGAGGGG 1620
Db 1561 CTCTGTGAACCCCTATGTGGAGGCGAAATGCTCTCCAGCCCTTGCAATTCAGAGGGG 1620
Qy 1621 CCCATGAAGAGGACAGGCTACCCCTTTTCAATAGAAATTTGAGCATCAGTGAAGTTAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTTCAATAGAAATTTGAGCATCAGTGAAGTTAA 1680
Qy 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTTGGGATCACTGATGA 1740
Db 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTTGGGATCACTGATGA 1740
Qy 1741 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCGCCCTCACACAGCCCTGGCCTCTGCT 1800
Db 1741 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCGCCCTCACACAGCCCTGGCCTCTGCT 1800
Qy 1801 CAACTAGCAGATACAGGAGTACGACCTGACTCTCTTAAAGGAGGCTGAGAGGCCAAA 1860
Db 1801 CAACTAGCAGATACAGGAGTACGACCTGACTCTCTTAAAGGAGGCTGAGAGGCCAAA 1860
Qy 1861 CTGCTGTCTCCAAACATGCACTTCTTCTTGAAGTATGTAAGCAAGTCCCTGCCATT 1920
Db 1861 CTGCTGTCTCCAAACATGCACTTCTTCTTGAAGTATGTAAGCAAGTCCCTGCCATT 1920
Qy 1921 GGAGAGAAAACTTAAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1980
Db 1921 GGAGAGAAAACTTAAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1980
Qy 1981 AATAATCTCTGTTAATATGTTGATCATTTCTTCTGATTAATTTCTACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATCATTTCTTCTGATTAATTTCTACATACATGTA 2040
Qy 2041 AATATGCTCTCTTTTAAATAGGTTGATCTATGCTGTTATGATGCTTTTATGAT 2100
Db 2041 AATATGCTCTCTTTTAAATAGGTTGATCTATGCTGTTATGATGCTTTTATGAT 2100
Qy 2101 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAACAGCAAAAAA 2160
Db 2101 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAACAGCAAAAAA 2160
Qy 2161 AAAAAA 2220
Db 2161 AAAAAA 2220
Qy 2221 AAAAAA 2261
Db 2221 AAAAAA 2261

RESULT 4
US-10-723-860-5746
; Sequence 5746, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5746
; LENGTH: 2134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-5746

Query Match 91.2%; Score 2061.6; DB 9; Length 2134;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2130; Conservative 0; Mismatches 4; Indels 46; Gaps 2;

Qy 1 GAAATCAGGCTCCGGCGCGGCGGAGGGGCGAACTTTCCCTCTGGCGCGCCACCGGCT 60
Db 1 GAAATCAGGCTCCGGCGCGGCGGCGGAGGGGCGAACTTTCCCTCTGGCGCGCCACCGGCT 60
Qy 61 CCGCGCGCCTCCCTCGCGCGCGGAGCTTTCGAGCCAAAGCAGCGTCTCTGGGAGCGGTCA 120
Db 61 CCGCGCGCCTCCCTCGCGCGCGGAGCTTTCGAGCCAAAGCAGCGTCTCTGGGAGCGGTCA 120
Qy 121 TGCCCTTACAGTACCGGCTTTGCTCTGCGCGCTGGCTTGTCTTCCACGCGCCAGGC 180
Db 121 TGCCCTTACAGTACCGGCTTTGCTCTGCGCGCTGGCTTGTCTTCCACGCGCCAGGC 180
Qy 181 CGAGCCAGTTCGGGTGTGCGCGCTGGATTCGAACTTGGAACTGGAGCGAGAGTGGAGC 240
Db 181 CGAGCCAGTTCGGGTGTGCGCGCTGGATTCGAACTTGGAACTGGAGCGAGAGTGGAGC 240
Qy 241 TGAAGTCCAGGTGTCTGTCCAAACCGAGCGTCCGGGTGCTCTGCGCGCTTCCAGCCGC 300
Db 241 TGAAGTCCAGGTGTCTGTCCAAACCGAGCGTCCGGGTGCTCTGCGCGCTTCCAGCCGC 300
Qy 301 GCGCGCGCGCGCGAGTCCCACTTCTCTATATCTTCCCAAAACAGCCCAAGCGCGG 360
Db 301 GCGCGCGCGCGCGAGTCCCACTTCTCTATATCTTCCCAAAACAGCCCAAGCGCGG 360
Qy 361 CCGAGGGCTGGAACACCCAGCGGTTCTCGGGCAAGAGGTTCGGGGGACACCTTCGCTCTCA 420
Db 361 CCGAGGGCTGGA-----CA 375
Qy 421 CCCTCAGAGCACTTCGCGCGAGAGACAGGCGTACTATTTCTGCTCGCGCTTCCAGCACT 480
Db 376 CCCTCAGAGCACTTCGCGCGAGAGACAGGCGTACTATTTCTGCTCGCGCTTCCAGCACT 435
Qy 481 CCATCATGTACTTCAGCCACTTTCGTCGCGGTCTTCTCCAGCGAAGCCACACGACGC 540
Db 436 CCATCATGTACTTCAGCCACTTTCGTCGCGGTCTTCTCCAGCGAAGCCACACGACGC 495
Qy 541 CAGCGCGCGGACACCAACACCGCGCGCCACCATCGGTGCGAGCCCTTGTCTCTCGCGC 600
Db 496 CAGCGCGCGGACACCAACACCGCGCGCCACCATCGGTGCGAGCCCTTGTCTCTCGCGC 555
Qy 601 CAGAGCGCTGCGCGCGCGGCGGCGAGTGCACACGAGGGGGTGGACTTCGCT 660
Db 556 CAGAGCGCTGCGCGCGCGGCGGCGGCGAGTGCACACGAGGGGGTGGACTTCGCT 615
Qy 661 GTGATATCTACATCTGGCGCGCTTTCGGCGGGGACTTTCGCGGGTCTTCTCTGTCACTGG 720
Db 616 GTGATATCTACATCTGGCGCGCTTTCGGCGGGGACTTTCGCGGGTCTTCTCTGTCACTGG 675
Qy 721 TTATCACCCCTTACTGCAACACCAAGAACCGAAGACGTGTTTGGAAATGTCCCCCGCTG 780
Db 676 TTATCACCCCTTACTGCAACACCAAGAACCGAAGACGTGTTTGGAAATGTCCCCCGCTG 735
Qy 781 TGGTCAATTCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG 840
Db 736 TGGTCAATTCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAG 795

QY 841 CCACATCACTTCAACTCAGAGTCCCTTCTTTGAGGGAGCAAGTCCCTTCCCTTCAT 900
Db 796 CCACATCACTTCAACTCAGAGTCCCTTCTTTGAGGGAGCAAGTCCCTTCCCTTCAT 855
QY 901 TTTTTCAGTCTTCTCCTCTGTATTCAATCTCATGATTAATTTTAGTGGGGGGGG 960
Db 856 TTTTTCAGTCTTCTCCTCTGTATTCAATCTCATGATTAATTTTAGTGGGGGGGG 915
QY 961 GTGGGAAGATTACTTTTCTTTATGTGTTTGAAGGGGAAACAAACTAGGTAAATCTAC 1020
Db 916 GTGGGAAGATTACTTTTCTTTATGTGTTTGAAGGGGAAACAAACTAGGTAAATCTAC 975
QY 1021 AGTACACCAAGGGTCAATATCTGTGCGGCACATCGGCTAGGCGTGGAAAGGG 1080
Db 976 AGTACACCAAGGGTCAATATCTGTGCGGCACATCGGCTAGGCGTGGAAAGGG 1035
QY 1081 CAGGCGAGAGTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGTGGAGGCCACCATG 1140
Db 1036 CAGGCGAGAGTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGTGGAGGCCACCATG 1095
QY 1141 CCATCTCAACCTCTTCCCGCCCGTTTTCACAAAGGGGAGGCTAAAGCCCAAGACAGCT 1200
Db 1096 CCATCTCAACCTCTTCCCGCCCGTTTTCACAAAGGGGAGGCTAAAGCCCAAGACAGCT 1155
QY 1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
Db 1156 TGATCAAAAGGCACACAGCAAGTCAAGGTTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1215
QY 1261 GCTCAGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG 1320
Db 1216 GCTCAGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG 1275
QY 1321 TGAGGTGTTGAGTCTCAACGGCAAGGAACAAGTACTTCTTGATCCTGGGATCTGT 1380
Db 1276 TGAGGTGTTGAGTCTCAACGGCAAGGAACAAGTACTTCTTGATCCTGGGATCTGT 1335
QY 1381 GCCAGAGCCTCGAGGAGTAAAGAAATTAAGAGAGAGTGCCTTTGGCAGAGTCTAT 1440
Db 1336 GCCAGAGCCTCGAGGAGTAAAGAAATTAAGAGAGAGTGCCTTTGGCAGAGTCTAT 1395
QY 1441 AATGTAAACAATATCAGACTTTTCTTTTATATCAAGCCTAAATTTGATAGACTAA 1500
Db 1396 AATGTAAACAATATCAGAC- TTTTCTTTTATATCAAGCCTAAATTTGATAGACTAA 1454
QY 1501 AATAAATGAAGTGTAGCTTAACCCCTGGAAATGAATCCCTCATCTCTAAAGAAAT 1560
Db 1455 AATAAATGAAGTGTAGCTTAACCCCTGGAAATGAATCCCTCATCTCTAAAGAGAT 1514
QY 1561 CTCTGTGAACCCCTATGTGAGGCGGAATGCTCTCCAGCCCTTGCAATTCGAGAGGG 1620
Db 1515 CTCTGTGAACCCCTATGTGAGGCGGAATGCTCTCCAGCCCTTGCAATTCGAGAGGG 1574
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1575 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTTAAA 1634
QY 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA 1740
Db 1635 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATGA 1694
QY 1741 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACAGCCCTTGGCTCTGCT 1800
Db 1695 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACAGCCCTTGGCTCTGCT 1754
QY 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Db 1755 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1814
QY 1861 CTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGTTAAGCAATGCTGCCCAT 1920
Db 1815 CTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGTTAAGCAATGCTGCCCAT 1874
QY 1921 GGAGAGAAACCTTAAAGTAGTAAGAAATGAAGAACCACTCATATTTCTTCACTTAG 1980

Db 1875 GGAGAGAAAAAATTAAAGTAGTAAGAAATGAAGAACCACTCATATTTCTTCACTTAG 1934
QY 1981 AATAATCTCCTGTTAAATATGTTGATCAATTTCTCCTGATTAATTTTACACATACATGAA 2040
Db 1935 AATAATCTCCTGTTAAATATGTTGATCAATTTCTCCTGATTAATTTTACACATACATGAA 1994
QY 2041 AATATGCTTCTTTTAAATAGGTTGATCTATGCTGTTATGATGGCTTTAATGAAT 2100
Db 1995 AATATGCTTCTTTTAAATAGGTTGATCTATGCTGTTATGATGGCTTTAATGAAT 2054
QY 2101 AAACATTTGTAGCATCTCTTTAATGTTAAACAGCAAAAAAATAAAAAA 2160
Db 2055 AAACATTTGTAGCATCTCTTTAATGTTAAACAGCAAAAAAATAAAAAA 2114
QY 2161 AAAAAAATAAAAAA 2180
Db 2115 AAAAAAATAAAAAA 2134

RESULT 5
US-10-804-762-4
; Sequence 4, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allo-rejection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-4

Query Match 89.7%; Score 2029; DB 9; Length 2150;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 2150; Conservative 0; Mismatches 0; Indels 111; Gaps 1;

QY 1 GAAATCAGGCTCCGGGCGCGCGAAGGGCGCAACTTTCCCGCTCGGCGCCCAACCGGT 60
Db 1 GAAATCAGGCTCCGGGCGCGCGAAGGGCGCAACTTTCCCGCTCGGCGCCCAACCGGT 60
QY 61 CCGCGGCGCTCCCTCGCGCCGAGCTTCGAGCCAAGAGGCTCCTGGGAGCGGTCA 120
Db 61 CCGCGGCGCTCCCTCGCGCCGAGCTTCGAGCCAAGAGGCTCCTGGGAGCGGTCA 120
QY 121 TGGCTTACAGTCAAGCCCTTGTCTCGCGCTGGCTTGTCTCCAGCCCGCAGG 180
Db 121 TGGCTTACAGTCAAGCCCTTGTCTCGCGCTGGCTTGTCTCCAGCCCGCAGG 180
QY 181 CGAGCGAGTTCGGGTGTCGCGCTGGATCGGAACTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCGAGTTCGGGTGTCGCGCTGGATCGGAACTGGGCGAGACAGTGGAGC 240
QY 241 TGAAGTCCAGGTGCTGTCTCAAACCGAGCTTCGCGGTGCTGTCTCGCGCGCAG 300
Db 241 TGAAGTCCAGGTGCTGTCTCAAACCGAGCTTCGCGGTGCTGTCTCGCGCGCAG 300
QY 301 GCGGCGCGCGCAGTCCCACTTCTCTATACCTCCCAAAACAGGCCCAAGGCGG 360
Db 301 GCGGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAACAGGCCCAAGGCGG 360
QY 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGACACCTTCGCTCA 420
Db 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGACACCTTCGCTCA 420

QY 421 CCTGAGCGACTTCCGCCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACT 480
DB 421 CCTGAGCGACTTCCGCCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACT 480
QY 481 CCATCATGTACTTCAGCCACTTGTGTCGGTCTTCTGCGAGGGAAGCCACACAGACGC 540
DB 481 CCATCATGTACTTCAGCCACTTGTGTCGGTCTTCTGCGAGGGAAGCCACACAGACGC 540
QY 541 CAGCGCGCGACACCAACACCGCGGCCCAACCATCGCGTCGACGCCCTGTCCCTGCGCC 600
DB 541 CAGCGCGCGACACCAACACCGCGGCCCAACCATCGCGTCGACGCCCTGTCCCTGCGCC 600
QY 601 CAGAGCGGTGCGCGCGCAGCGCGGGGGGCGAGTGCCACACGAGGGGGCTGGACTTCGCGCT 660
DB 601 CAGAGCGGTGCGCGCGCAGCGCGGGGGGCGAG----- 633
QY 661 GTGATATCTACATCTGGGCGCCCTGGCGCGGACCTGTGGGGTCTTCTCCTGTCACTGG 720
DB 634 ----- 633
QY 721 TTATCAACCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAACTGTCCCGGCCCTG 780
DB 634 -----GGAACCGAAGACGTGTTTGCAAACTGTCCCGGCCCTG 669
QY 781 TGGTCAAAATCGGAGACAAAGCCAGCCTTTTCGGCGAGATACGTCCTAAACCCTGTGCAACAG 840
DB 670 TGGTCAAAATCGGAGACAAAGCCAGCCTTTTCGGCGAGATACGTCCTAAACCCTGTGCAACAG 729
QY 841 CCACTACATTAATTCNAACCTGAGATCCTTCCTTTTGGGGAGCAAGTCCTCCCTTTGAT 900
DB 730 CCACTACATTAATTCNAACCTGAGATCCTTCCTTTTGGGGAGCAAGTCCTCCCTTTGAT 789
QY 901 TTTTTCACGCTCTTCCCTGCTGATTCATTCCTCATGATTAATTTAGTGGGGCGGG 960
DB 790 TTTTTCACGCTCTTCCCTGCTGATTCATTCCTCATGATTAATTTAGTGGGGCGGG 849
QY 961 GTGGAAAGATTAATTTTCTTTATGTGTTTCAACGGGAAACAAAACCTAGGTAAATCTAC 1020
DB 850 GTGGAAAGATTAATTTTCTTTATGTGTTTCAACGGGAAACAAAACCTAGGTAAATCTAC 909
QY 1021 AGTACACCAAGGGTCAAAATACTGTTGTGCGCACATCGCGTAGGGGTGGAAGGG 1080
DB 910 AGTACACCAAGGGTCAAAATACTGTTGTGCGCACATCGCGTAGGGGTGGAAGGG 969
QY 1081 CAGGCGCAGAGCTACCGCAGAGTCTCTCAGAATCATGCTCAGAGAGCTGGAGGCACCCATG 1140
DB 970 CAGGCGCAGAGCTACCGCAGAGTCTCTCAGAATCATGCTCAGAGAGCTGGAGGCACCCATG 1029
QY 1141 CCATCTCAACCTTTCCCGCCCGTTTACAAAGGGGAGGCTAAAGCCCGAGAGACAGCT 1200
DB 1030 CCATCTCAACCTTTCCCGCCCGTTTACAAAGGGGAGGCTAAAGCCCGAGAGACAGCT 1089
QY 1201 TGATCAAAAGGCAACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
DB 1090 TGATCAAAAGGCAACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCA 1149
QY 1261 GCTCAGGCTCTTTCTCCACACCATTCAGGCTCTTCTTCCGAGGCCCTGTCTCAGGG 1320
DB 1150 GCTCAGGCTCTTTCTCCACACCATTCAGGCTCTTCTTCCGAGGCCCTGTCTCAGGG 1209
QY 1321 TGAGGTGCTTGAAGTCTCAACCGCGCAAGGGAACAAGTACTTCTTGTATACCTGGGATACTGT 1380
DB 1210 TGAGGTGCTTGAAGTCTCAACCGCGCAAGGGAACAAGTACTTCTTGTATACCTGGGATACTGT 1269
QY 1381 GCCCAGAGCCTCGAGAGGTAATGAATTAAGAAGAGAACTCCCTTTGGCAGAGTTCTAT 1440
DB 1270 GCCCAGAGCCTCGAGAGGTAATGAATTAAGAAGAGAACTCCCTTTGGCAGAGTTCTAT 1329
QY 1441 AATGTAAACAATATCAGACTTTTCTTTTATTAATCAAGCCCTAAATTTGTATAGACCTAA 1500
DB 1330 AATGTAAACAATATCAGACTTTTCTTTTATTAATCAAGCCCTAAATTTGTATAGACCTAA 1389

QY 1501 AATAAAATGAAGTGTGAGCTTTAAACCTGGAATAATGAATCCCTCTATCTCTAAAGAAAAT 1560
DB 1390 AATAAAATGAAGTGTGAGCTTTAAACCTGGAATAATGAATCCCTCTATCTCTAAAGAAAAT 1449
QY 1561 CTCTGTGAAAACCCCTATATGAGGAGGGAATGCTCTCCAGGCCCTTGCATGTCAGAGGGG 1620
DB 1450 CTCTGTGAAAACCCCTATATGAGGAGGGAATGCTCTCCAGGCCCTTGCATGTCAGAGGGG 1509
QY 1621 CCATGAAAGAGACAGGCTACCCCTTTTACAAATAGAATTTGAGCATCAGTGAGGTTAAA 1680
DB 1510 CCATGAAAGAGACAGGCTACCCCTTTTACAAATAGAATTTGAGCATCAGTGAGGTTAAA 1569
QY 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 1740
DB 1570 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 1629
QY 1741 CTTTTTATACCTTTTAAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCTCTGCT 1800
DB 1630 CTTTTTATACCTTTTAAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCTCTGCT 1689
QY 1801 CAACTAGCAGATACAGGGATGAGGACCTGACTCTCTCTTAAGGAGGCTGAGAGCCCAA 1860
DB 1690 CAACTAGCAGATACAGGGATGAGGACCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1749
QY 1861 CTGCTGTCCCAACATGCACCTTCTTGTCTTAAGGTATGTCACAAAGCAATGCCTGCCAT 1920
DB 1750 CTGCTGTCCCAACATGCACCTTCTTGTCTTAAGGTATGTCACAAAGCAATGCCTGCCAT 1809
QY 1921 GGAGAGAAAAACTTAAGTAGATAGGAAATAGAAACCACTCATTAATTTCTTCACTTAGG 1980
DB 1810 GGAGAGAAAAACTTAAGTAGATAGGAAATAGAAACCACTCATTAATTTCTTCACTTAGG 1869
QY 1981 AATAATCTCTCTTAATATGTTGATACATTTCTTCTGATTTATTTCTTACACATACATGTA 2040
DB 1870 AATAATCTCTCTTAATATGTTGATACATTTCTTCTGATTTATTTCTTACACATACATGTA 1929
QY 2041 AATATGCTCTTTCTTTTAAATAGGGTTGTACTATGCTGTATGAGTGGCTTTTAAATGAAT 2100
DB 1930 AATATGCTCTTTCTTTTAAATAGGGTTGTACTATGCTGTATGAGTGGCTTTTAAATGAAT 1989
QY 2101 AAACATTTGTAGCATCCTTTTAAAGGGTAAACACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2160
DB 1990 AAACATTTGTAGCATCCTTTTAAAGGGTAAACACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2049
QY 2161 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
DB 2050 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2109
QY 2221 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2261
DB 2110 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2150

RESULT 6

US-10-804-763-4
; Sequence 4, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-804-763-4

| | | | | | |
|-----------------------|-----|--|---------------|-------------|--------------|
| Query Match | | 89.7%; | Score 2029; | DB 10; | Length 2150; |
| Best Local Similarity | | 95.1%; | Pred. No. 0; | | |
| Matches 2150; | | Conservative 0; | Mismatches 0; | Indels 111; | Gaps 1; |
| Qy | 1 | GAATCAGGCTCCGGGCGGCGGCGAAGGGCGCAACTTTCCCTCCGCGGCGCCCAACCGGCT | 60 | | |
| Db | 1 | GAATCAGGCTCCGGGCGGCGGCGAAGGGCGCAACTTTCCCTCCGCGGCGCCCAACCGGCT | 60 | | |
| Qy | 61 | CCGCGCGGCTCCCTCGCGCCGAGCTTCAGAGCAAGCAGCGTCCTGGGAGCGGTCA | 120 | | |
| Db | 61 | CCGCGCGGCTCCCTCGCGCCGAGCTTCAGAGCAAGCAGCGTCCTGGGAGCGGTCA | 120 | | |
| Qy | 121 | TGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCTCAACGCCCAAGC | 180 | | |
| Db | 121 | TGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCTCAACGCCCAAGC | 180 | | |
| Qy | 181 | CGAGCCAGTTCGGGCTCGCGCTGGATCGGATCGGACCTGGGCGAGACAGTGGAGC | 240 | | |
| Db | 181 | CGAGCCAGTTCGGGCTCGCGCTGGATCGGATCGGACCTGGGCGAGACAGTGGAGC | 240 | | |
| Qy | 241 | TGAAGTCCAGTGTCTGTCTCAACCGAGCTCGGGCTGTCTGTGGCTCTTCAGCGCG | 300 | | |
| Db | 241 | TGAAGTCCAGTGTCTGTCTCAACCGAGCTCGGGCTGTCTGTGGCTCTTCAGCGCG | 300 | | |
| Qy | 301 | CGGCGCGCGCGCAGTCCCACTTCCTCTATACCTCTCCCAAAACAAAGCCCAAGCGG | 360 | | |
| Db | 301 | CGGCGCGCGCGCAGTCCCACTTCCTCTATACCTCTCCCAAAACAAAGCCCAAGCGG | 360 | | |
| Qy | 361 | CGAGGGGCTGGACACCGAGGGTTCCTGGGCAAGAGTTCGGGACACCTTCGTCCTCA | 420 | | |
| Db | 361 | CGAGGGGCTGGACACCGAGGGTTCCTGGGCAAGAGTTCGGGACACCTTCGTCCTCA | 420 | | |
| Qy | 421 | CCCTGAGCGACTTCGCGCGAGAGCAGAGGCTACTATTCTGCTCGGCCCTGAGCAACT | 480 | | |
| Db | 421 | CCCTGAGCGACTTCGCGCGAGAGCAGAGGCTACTATTCTGCTCGGCCCTGAGCAACT | 480 | | |
| Qy | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGCTTCCTGCCAGCGAAGCCCAACGACGC | 540 | | |
| Db | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGCTTCCTGCCAGCGAAGCCCAACGACGC | 540 | | |
| Qy | 541 | CAGCGCGGACACACACCGGGCGCCACATCGCTCGGCGAGCCCTGCTCGGCC | 600 | | |
| Db | 541 | CAGCGCGGACACACACCGGGCGCCACATCGCTCGGCGAGCCCTGCTCGGCC | 600 | | |
| Qy | 601 | CAGAGGCTCGCGCGAGCGCGGGCGCAGTGCACACGAGGGGGCTGGACTTCGGCT | 660 | | |
| Db | 601 | CAGAGGCTCGCGCGAGCGCGGGCGCAGTGCACACGAGGGGGCTGGACTTCGGCT | 660 | | |
| Qy | 661 | GTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACCTGG | 720 | | |
| Db | 634 | ----- | 633 | | |
| Qy | 721 | TTATCACCCCTTACTGCAACACACAGGACCGAAGACGTGTTGCAATGTCCCGGCGCTG | 780 | | |
| Db | 634 | -----GGAACCGAAGACGTGTTGCAATGTCCCGGCGCTG | 669 | | |
| Qy | 781 | TGGTCAAAATCGGAGACAAAGCCCTTCGGCGAGATACGCTTAAACCTGTGCAACAG | 840 | | |
| Db | 670 | TGGTCAAAATCGGAGACAAAGCCCTTCGGCGAGATACGCTTAAACCTGTGCAACAG | 729 | | |
| Qy | 841 | CCACTACATTACTTCAAACTGAGATCTTCCTTTTGGGAGCAAGTCCCTCCCTTCAT | 900 | | |
| Db | 730 | CCACTACATTACTTCAAACTGAGATCTTCCTTTTGGGAGCAAGTCCCTCCCTTCAT | 789 | | |
| Qy | 901 | TTTTTCCAGTCTCTCCCTGTGATTCATCTCATGATTAATTTTGTGGGGCGGG | 960 | | |
| Db | 790 | TTTTTCCAGTCTCTCCCTGTGATTCATCTCATGATTAATTTTGTGGGGCGGG | 849 | | |
| Qy | 961 | GTGGAAAGATTACTTTTTTCTTATGTGTTTGGCGGAAACAAAACTAGGTAAATCTAC | 1020 | | |
| Db | 850 | GTGGAAAGATTACTTTTTTCTTATGTGTTTGGCGGAAACAAAACTAGGTAAATCTAC | 909 | | |

| | | | | | |
|----|------|---|------|--|--|
| Qy | 1021 | AGTACACCAAGGGTCAAACTACTGTGTGCGCAATCGCGGTAGGCGGTGAAAAGGGG | 1080 | | |
| Db | 910 | AGTACACCAAGGGTCAAACTACTGTGTGCGCAATCGCGGTAGGCGGTGAAAAGGGG | 969 | | |
| Qy | 1081 | CAGCCAGAGTACCCCGAGGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCAACCCATG | 1140 | | |
| Db | 970 | CAGCCAGAGTACCCCGAGGTTCTCAGAAATCATGCTGAGAGAGCTGGAGGCAACCCATG | 1029 | | |
| Qy | 1141 | CCATCTCAAACCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCCAAGACAGCT | 1200 | | |
| Db | 1030 | CCATCTCAAACCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCCAAGACAGCT | 1089 | | |
| Qy | 1201 | TGATCAAAGGCAACAGCAAGTCAAGGTTGAGAGAGTAGCTGGAGGACCTTGTCTCCA | 1260 | | |
| Db | 1090 | TGATCAAAGGCAACAGCAAGTCAAGGTTGAGAGAGTAGCTGGAGGACCTTGTCTCCA | 1149 | | |
| Qy | 1261 | GCTCAGGCTCTTTCCTCCACACCATTCAGGTCTTTTCCGAGGCGCCCTGTCTCAGGG | 1320 | | |
| Db | 1150 | GCTCAGGCTCTTTCCTCCACACCATTCAGGTCTTTTCCGAGGCGCCCTGTCTCAGGG | 1209 | | |
| Qy | 1321 | TGAGTCTTGTAGTCTCCAAAGGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT | 1380 | | |
| Db | 1210 | TGAGTCTTGTAGTCTCCAAAGGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT | 1269 | | |
| Qy | 1381 | GCCAGAGCTCGAGGAGGTAATGAATTAAGAGAGAGACTGCCCTTTGGCAGAGTCTAT | 1440 | | |
| Db | 1270 | GCCAGAGCTCGAGGAGGTAATGAATTAAGAGAGAGACTGCCCTTTGGCAGAGTCTAT | 1329 | | |
| Qy | 1441 | AATCTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGATATAGACTAA | 1500 | | |
| Db | 1330 | AATCTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGATATAGACTAA | 1389 | | |
| Qy | 1501 | AATAAAAAGAGTGGTGAAGTAAACCTCGGAAAAATGAATCCCTCTATCTCTAAAGAAAT | 1560 | | |
| Db | 1390 | AATAAAAAGAGTGGTGAAGTAAACCTCGGAAAAATGAATCCCTCTATCTCTAAAGAAAT | 1449 | | |
| Qy | 1561 | CTCTGTAAACCCCTATGTGGAGGGGAAATGTCTCTCCAGCCCTTGATGTCAGAGGG | 1620 | | |
| Db | 1450 | CTCTGTAAACCCCTATGTGGAGGGGAAATGTCTCTCCAGCCCTTGATGTCAGAGGG | 1509 | | |
| Qy | 1621 | CCCATGAAGAGGACAGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAGGTAAA | 1680 | | |
| Db | 1510 | CCCATGAAGAGGACAGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAGGTAAA | 1569 | | |
| Qy | 1681 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA | 1740 | | |
| Db | 1570 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA | 1629 | | |
| Qy | 1741 | CTTTTATATCTTTGTAAGACAATTTGAGAGGCGCCCTCACAGCCCTGGCCTCTGCT | 1800 | | |
| Db | 1630 | CTTTTATATCTTTGTAAGACAATTTGAGAGGCGCCCTCACAGCCCTGGCCTCTGCT | 1689 | | |
| Qy | 1801 | CAACTAGCAGATACAGGATGAGGACCTGACTCTCTTAAGGAGGCTGAGAGCCCAAA | 1860 | | |
| Db | 1690 | CAACTAGCAGATACAGGATGAGGACCTGACTCTCTTAAGGAGGCTGAGAGCCCAAA | 1749 | | |
| Qy | 1861 | CTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGGTACAAACAATGCTGCCATTT | 1920 | | |
| Db | 1750 | CTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGGTACAAACAATGCTGCCATTT | 1809 | | |
| Qy | 1921 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTTCAACCTTAGG | 1980 | | |
| Db | 1810 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTTCAACCTTAGG | 1869 | | |
| Qy | 1981 | AATAATCTCTGTTAAATATGTTGATACATTTCTTCTGATTTATTTTCTACACATACATGTA | 2040 | | |
| Db | 1870 | AATAATCTCTGTTAAATATGTTGATACATTTCTTCTGATTTATTTTCTACACATACATGTA | 1929 | | |
| Qy | 2041 | AATAATCTCTTTTAAATAGGGTTGATATGCTGTTTATGATGCTGCTTTTAAATGAAAT | 2100 | | |
| Db | 1930 | AATAATCTCTTTTAAATAGGGTTGATATGCTGCTTTTATGATGCTGCTTTTAAATGAAAT | 1989 | | |

| | | | |
|----|------|--|------|
| Qy | 2101 | AAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2160 |
| Db | 1990 | AAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2049 |
| Qy | 2161 | AA | 2220 |
| Db | 2050 | AA | 2109 |
| Qy | 2221 | AA | 2261 |
| Db | 2110 | AA | 2150 |

RESULT 7

US-10-723-860-1243

; Sequence 1243, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NFUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1243

; LENGTH: 1729

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-860-1243

| | | | | |
|----|------|--|---|-----|
| Db | 767 | | GCTCGAGGAGCATTGTCTCCAGCTCAGGGCTCTTTCTCCACACCAATTCAGTGCTTTCT | 826 |
| Qy | 1299 | TTCCGAGGCCCTGTCTCAGGTGAGTGCTTGAGTCTCCAAAGCGCAAGGMAACAAGTAC | 1358 | |
| Db | 827 | TTCCGAGGCCCTGTCTCAGGTGAGTGCTTGAGTCTCCAAAGCGCAAGGMAACAAGTAC | 886 | |
| Qy | 1359 | TTCTTGATACCTGGGATACCTGTGCCAGAGCCTCGAGAGGTAAATGAATAAAGAAGAGA | 1418 | |
| Db | 887 | TTCTTGATACCTGGGATACCTGTGCCAGAGCCTCGAGAGGTAAATGAATAAAGAAGAGA | 946 | |
| Qy | 1419 | ACTGCCCTTTGGCAGAGTTCTATAATGTAAACAATATCAGACTTTTTTTTTTATAATCAA | 1478 | |
| Db | 947 | ACTGCCCTTTGGCGAAGTTCTATAATGTAAACAATATCAGACTTTTTTTTTTATAATCAA | 1006 | |
| Qy | 1479 | GCCTAAAAATGTATAGACCTAAATAAAATGAAGTGTGAGCTTAACCCCTGGAAAAATGAA | 1538 | |
| Db | 1007 | GCCTAAAAATGTATAGACCTAAATAAAATGAAGTGTGAGCTTAACCCCTGGAAAAATGAA | 1066 | |
| Qy | 1539 | TCCCTCTATCTCTAAAGAAAATCTCTGTGAAGCCCTATCTGGAGGCGGAATTGCTCTCC | 1598 | |
| Db | 1067 | TCCCTCTATCTCTAAAGAAAATCTCTGTGAAGCCCTATCTGGAGGCGGAATTGCTCTCC | 1126 | |
| Qy | 1599 | CAGCCCTTGCAATGCGAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTACAATAGAA | 1658 | |
| Db | 1127 | CAGCCCTTGCAATGCGAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTACAATAGAA | 1186 | |
| Qy | 1659 | TTTGAGCATCAGTGAGGTAAACTTAAGGCCCTCTTTGAATCTCTGAATTTTGAGATACAAAC | 1718 | |
| Db | 1187 | TTTGAGCATCAGTGAGGTAAACTTAAGGCCCTCTTTGAATCTCTGAATTTTGAGATACAAAC | 1246 | |
| Qy | 1719 | ATGTTCTGGGATCAGTACCTTTTATATCTTTGTAAAGACAAATTTTGGAGAGCCCC | 1778 | |
| Db | 1247 | ATGTTCTGGGATCAGTACCTTTTATATCTTTGTAAAGACAAATTTTGGAGAGCCCC | 1306 | |
| Qy | 1779 | TCACAGAGCCCTGGCCTCTGCTCAACTAGCAGATACAGGATGAGGCAGACCTGACTCTC | 1838 | |
| Db | 1307 | TCACAGAGCCCTGGCCTCTGCTCAACTAGCAGATACAGGATGAGGCAGACCTGACTCTC | 1366 | |
| Qy | 1839 | TTAAGGAGGCTGAGAGGCCAAACTGCTGTGCCAAACATGCACATCTCTTGTCTTAAGGTATG | 1898 | |
| Db | 1367 | TTAAGGAGGCTGAGAGGCCAAACTGCTGTGCCAAACATGCACATCTCTTGTCTTAAGGTATG | 1426 | |
| Qy | 1899 | GTACAAGCAATGCTGCCCATTTGGAGAGAAAAAACTTAACTAGATAGGAAATAAGAACC | 1958 | |
| Db | 1427 | GTACAAGCAATGCTGCCCATTTGGAGAGAAAAAACTTAACTAGATAGGAAATAAGAACC | 1486 | |
| Qy | 1959 | ACTCATAAATCTTCACCTTAGGAATATCTCCTGTTTAATATGTTGATACATCTTCTCTGAT | 2018 | |
| Db | 1487 | ACTCATAAATCTTCACCTTAGGAATATCTCCTGTTTAATATGTTGATACATCTTCTCTGAT | 1546 | |
| Qy | 2019 | TATTTTCTACACATACATGTAAAAATATGCTTTCTTTTAAAAATAGGGTTGTACTATGCT | 2078 | |
| Db | 1547 | TATTTTCTACACATACATGTAAAAATATGCTTTCTTTTAAAAATAGGGTTGTACTATGCT | 1606 | |
| Qy | 2079 | GTTATAGTGCGCTTTTAATGAATAAACATTTGTAGCATCTCTTTTAATGGGTAAACAGCA | 2137 | |
| Db | 1607 | GTTATAGTGCGCTTTTAATGAATAAACATTTGTAGCATCTCTTTTAATGGGTAAACAGCA | 1665 | |

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RESULT 8
US-10-207-655-173
; Sequence 173, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 173
; LENGTH: 1060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-173

Query Match      46.4%; Score 1048; DB 6; Length 1060;
Best Local Similarity 100.0%; Pred. No. 5.6e-159;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 CGCTCCCTCGCGCCGAGCTTCGAGCCAGCAGCGTCTGGGAGCGGCTCATGGCCT 126
Db 13 CGCTTCCTTCGCGCCGAGCTTCGAGCCAGCAGCGTCTGGGAGCGGCTCATGGCCT 72
Qy 127 TACCAGTGACCGCTTGTCTCGCGTGGCTTGTCTCTCCACGCCGCCAGGCCGAGCC 186
Db 73 TACCAGTGACCGCTTGTCTCGCGTGGCTTGTCTCTCCACGCCGCCAGGCCGAGCC 132
Qy 187 AGTTCGGGTGTGCGCGTGGATCGGACCTGGAACTGGGCGAGACAGTGAAGT 246
Db 133 AGTTCGGGTGTGCGCGTGGATCGGACCTGGAACTGGGCGAGACAGTGAAGT 192
Qy 247 GCCAGGTGCTCTGTCCAAACCGAGCTCGGCTGTCTGTGGCTCTTCCAGCGCGCGCGC 306
Db 193 GCCAGGTGCTCTGTCCAAACCGAGCTCGGCTGTCTGTGGCTCTTCCAGCGCGCGCGC 252
Qy 307 CGCGCGCCAGTCCCACTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGCCGAGG 366
Db 253 CGCGCGCCAGTCCCACTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGCCGAGG 312
Qy 367 GGCTGGACACCCAGGGTTCCTGGGCAAGAGGTTGGGGGACACCTTGTCTCACCCTGA 426
Db 313 GGCTGGACACCCAGGGTTCCTGGGCAAGAGGTTGGGGGACACCTTGTCTCACCCTGA 372
Qy 427 GCGACTTCCGCGGAGAGAACGAGGCTACTATTTCTGTCTCGGCTCGGCAACTCCATCA 486
Db 373 GCGACTTCCGCGGAGAGAACGAGGCTACTATTTCTGTCTCGGCTCGGCAACTCCATCA 432
Qy 487 TGTACTTCAGCCACTTCGTGCGGCTTCCTGCGAGCGAGGCTGAGCTTCGCTGTGATA 546
Db 433 TGTACTTCAGCCACTTCGTGCGGCTTCCTGCGAGCGAGGCTGAGCTTCGCTGTGATA 492
Qy 547 CGCGACCAACACCCGCGGCCACCATCGGTCGCGACGCCCTGTCTGCGCGCCAGAGG 606
Db 493 CGCGACCAACACCCGCGGCCACCATCGGTCGCGACGCCCTGTCTGCGCGCCAGAGG 552
Qy 607 CGTGGCGCCAGCGCGCGGCGCGAGTGACACAGAGGGGCTGAGCTTCGCTGTGATA 666
Db 553 CGTGGCGCCAGCGCGCGGCGCGAGTGACACAGAGGGGCTGAGCTTCGCTGTGATA 612
Qy 667 TCTACATCTGGCGGCTTCGCGGAGCTTGTGGGGTCTTCTCTCTGTCACTGGTTATCA 726
Db 613 TCTACATCTGGCGGCTTCGCGGAGCTTGTGGGGTCTTCTCTCTGTCACTGGTTATCA 672
Qy 727 CCTTTACTGCAACACAGGACCGAAGACGTGTTTGCAATGTCTCCCGGCTGTGTCA 786
Db 673 CCTTTACTGCAACACAGGACCGAAGACGTGTTTGCAATGTCTCCCGGCTGTGTCA 732
Qy 787 AATCGGAGACAAGCCAGCCCTTCGCGGAGATAGTCTTAACCCCTGTGCAACAGCACCTA 846
Db 733 AATCGGAGACAAGCCAGCCCTTCGCGGAGATAGTCTTAACCCCTGTGCAACAGCACCTA 792
Qy 847 CATTACTTCAAACTGAGATCTTCTTTTGAGGGAGCAAGTCTTCCCTTTCATTTTTC 906
Db 793 CATTACTTCAAACTGAGATCTTCTTTTGAGGGAGCAAGTCTTCCCTTTCATTTTTC 852
Qy 907 CAGTCTTCTCCCTGTGTATTCATTTCTCATGATTAATTTTGTAGGGGGGGGTGGGA 966
Db 853 CAGTCTTCTCCCTGTGTATTCATTTCTCATGATTAATTTTGTAGGGGGGGGTGGGA 912
Qy 967 AAGATTACTTTTCTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTACAGTACA 1026
Db 913 AAGATTACTTTTCTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTACAGTACA 972
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Qy 1027 CCACAAGGTCACAATACTGTTGTGCGCACATCCGGTAGGCGCTGGAAGGGGCGAGCC 1086
Db 973 CCACAAGGTCACAATACTGTTGTGCGCACATCCGGTAGGCGCTGGAAGGGGCGAGCC 1032
Qy 1087 AGAGCTACCCGCGAGGTTCTCAGAATCA 1114
Db 1033 AGAGCTACCCGCGAGGTTCTCAGAATCA 1060

RESULT 9
US-10-641-643-1014
; Sequence 1014, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
;           Susan G. Stuart
;           Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179145
; SEQUENCE DESCRIPTION: SEQ ID NO: 1014 :
US-10-641-643-1014

Query Match      46.4%; Score 1048; DB 8; Length 1060;
Best Local Similarity 100.0%; Pred. No. 5.6e-159;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 CGCTCCCTCGCGCCGAGCTTCGAGCCAGCAGCGTCTGGGAGCGGCTCATGGCCT 126
Db 13 CGCTTCCTTCGCGCCGAGCTTCGAGCCAGCAGCGTCTGGGAGCGGCTCATGGCCT 72
Qy 127 TACCAGTGACCGCTTGTCTCGCGTGGCTTGTCTCTCCACGCCGCCAGGCCGAGCC 186
Db 73 TACCAGTGACCGCTTGTCTCGCGTGGCTTGTCTCTCCACGCCGCCAGGCCGAGCC 132
Qy 187 AGTTCGGGTGTGCGCGTGGATCGGACCTGGAACTGGGCGAGACAGTGAAGT 246
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Db 133 AGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAGCTGAAGT 192
QY 247 GCCAGGTGCTGCTGTCCAAACCCGACGCTGGGCTGCTGCTGGCTTCCAGACCGCGCGG 306
Db 193 GCCAGGTGCTGCTGTCCAAACCCGACGCTGGGCTGCTGCTGGCTTCCAGACCGCGCGG 252
QY 307 CGCGCGCAGTCCACCTTCTCTCTATACCTCTCTCCAAACAGCCCAAGCGGCGCGAGG 366
Db 253 CGCGCGCAGTCCACCTTCTCTCTATACCTCTCTCCAAACAGCCCAAGCGGCGCGAGG 312
QY 367 GCTGTGACACCCAGCGGCTTCTGGGCAAGAGTGGGGACACCTTCCTCCACCTCA 426
Db 313 GCTGTGACACCCAGCGGCTTCTGGGCAAGAGTGGGGACACCTTCCTCCACCTCA 372
QY 427 GCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAACTCCATCA 486
Db 373 GCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAACTCCATCA 432
QY 487 TGTACTTACGACCTTCTGTCGGCTTCTCTGCGAGCGAAGCCACCAAGCGCGAGCGC 546
Db 433 TGTACTTACGACCTTCTGTCGGCTTCTCTGCGAGCGAAGCCACCAAGCGCGAGCGC 492
QY 547 CGCGACCAACACCGCGCGCCACCATCGCTCGGAGCCCTGCTCCCTGCGCGCGAGGG 606
Db 493 CGCGACCAACACCGCGCGCCACCATCGCTCGGAGCCCTGCTCCCTGCGCGCGAGGG 552
QY 607 CGTGGCGGCGAGCGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCTGTGATA 666
Db 553 CGTGGCGGCGAGCGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCTGTGATA 612
QY 667 TCTACATCTGGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTGGTTATCA 726
Db 613 TCTACATCTGGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTGGTTATCA 672
QY 727 CCTTTTACTGCAACACAGGACCGAGAGCTTGTGCAAGTTCCTCGGCGCTGTGCTCA 786
Db 673 CCTTTTACTGCAACACAGGACCGAGAGCTTGTGCAAGTTCCTCGGCGCTGTGCTCA 732
QY 787 AATCGGAGACAAAGCCGCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCCACTA 846
Db 733 AATCGGAGACAAAGCCGCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCCACTA 792
QY 847 CATTACTTCAAACTGAGATCTTCTTTTGGGAGCAAGTCTTCCCTTTCATTTTTC 906
Db 793 CATTACTTCAAACTGAGATCTTCTTTTGGGAGCAAGTCTTCCCTTTCATTTTTC 852
QY 907 GAGTCTTCTGCTGTATTCATTTCTCATGATTATTTTGTGGGGCGGGTGGGA 966
Db 853 GAGTCTTCTGCTGTATTCATTTCTCATGATTATTTTGTGGGGCGGGTGGGA 912
QY 967 AAGATTACTTTTCTTTATGTGTGACGGGAAACAAAACTAGGTAAATCTACAGTACA 1026
Db 913 AAGATTACTTTTCTTTATGTGTGACGGGAAACAAAACTAGGTAAATCTACAGTACA 972
QY 1027 CCACAAGGTCACAACTGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC 1086
Db 973 CCACAAGGTCACAACTGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC 1032
QY 1087 AGAGTACCCGAGAGTTCTCAGATCA 1114
Db 1033 AGAGTACCCGAGAGTTCTCAGATCA 1060

RESULT 10

US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allorejection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)

; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Query Match 31.3%; Score 708; DB 9; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.7e-104;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATGGGCTTACCAAGTACCGGCTTGTCTGCTCCGCTGGCCCTTGTCTGCTCCAGCGCGCAGG 179
Db 1 ATGGGCTTACCAAGTACCGGCTTGTCTGCTCCGCTGGCCCTTGTCTGCTCCAGCGCGCAGG 60
QY 180 CCGAGCCAGTTCGGGCTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCGGGCTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120
QY 240 CTGAAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGTCTGCTGCTCTTCCAGCGG 299
Db 121 CTGAAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGTCTGCTGCTCTTCCAGCGG 180
QY 300 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAAAGCCCAAGGGCG 359
Db 181 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAAAGCCCAAGGGCG 240
QY 360 GCCGAGGGGCTGCGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTC 419
Db 241 GCCGAGGGGCTGCGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTC 300
QY 420 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 360
QY 480 TCCATCATGTACTTACGACACTTCTGTCGGGCTTCTGCGAGCGAAGCCACCGAGCG 539
Db 361 TCCATCATGTACTTACGACACTTCTGTCGGGCTTCTGCGAGCGAAGCCACCGAGCG 420
QY 540 CCAGCGCGCGACCAACACCGCGCCACCATCGGTCGCGAGCCCTGCTCCCTGCGC 599
Db 421 CCAGCGCGCGACCAACACCGCGCCACCATCGGTCGCGAGCCCTGCTCCCTGCGC 480
QY 600 CCAGAGGGGCTGCGCGCGAGCGCGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCGC 659
Db 481 CCAGAGGGGCTGCGCGCGAGCGCGGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCGC 540
QY 660 TGTGATATCATCTGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 719
Db 541 TGTGATATCATCTGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 600
QY 720 GTTATCACTTCTTACTGCAACACAGGAAACGAGACGCTGTTGCAAAATGCTCCCGGCT 779
Db 601 GTTATCACTTCTTACTGCAACACAGGAAACGAGACGCTGTTGCAAAATGCTCCCGGCT 660
QY 780 GTGTCATAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTCTAA 827
Db 661 GTGTCATAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTCTAA 708

RESULT 11

US-10-804-763-28
; Sequence 28, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula

```
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-28

Query Match      31.3%; Score 708; DB 10; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.7e-104;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 ATGGCTTACAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCGAGG 179
Db 1 ATGGCTTACAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCGAGG 60

Qy 180 CCGAGCCAGTTCGGGTGTCGCGTGGATCGGACCTGGAACCTGGGGGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCGGGTGTCGCGTGGATCGGACCTGGAACCTGGGGGAGACAGTGGAG 120

Qy 240 CTGAAGTGCCAGGTGCTCTGTCCAAACCCGACGTGGGCTGTCTCGTGGCTTTCCAGCG 299
Db 121 CTGAAGTGCCAGGTGCTCTGTCCAAACCCGACGTGGGCTGTCTCGTGGCTTTCCAGCG 180

Qy 300 CGCGGCGCGCGCGGACGTCACCTTCTCTCTATACCTCTCCAAAAAAGCCCAAGCG 359
Db 181 CGCGGCGCGCGCGGACGTCACCTTCTCTCTATACCTCTCCAAAAAAGCCCAAGCG 240

Qy 360 GCCGAGGGGTGGACACCCAGCGGTTCTCGGCAAGAGTGGGGGACACCTTGTCTCTC 419
Db 241 GCCGAGGGGTGGACACCCAGCGGTTCTCGGCAAGAGTGGGGGACACCTTGTCTCTC 300

Qy 420 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGGCCCTTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGGCCCTTGAGCAAC 360

Qy 480 TCCATATGTACTTACGACACTTCTGTCGGGTCTTCTGCGACGAGAACCCACACGACG 539
Db 361 TCCATATGTACTTACGACACTTCTGTCGGGTCTTCTGCGACGAGAACCCACACGACG 420

Qy 540 CCAGCGCGGACCAACCAACCGCGCCACCATCGGTGCGAGCGCTGTCCCTGCGC 599
Db 421 CCAGCGCGGACCAACCAACCGCGCCACCATCGGTGCGAGCGCTGTCCCTGCGC 480

Qy 600 CCAGAGGCGTGC CGGCCAGCGCGGGGGCGGCGAGTGCAACAGAGGGGCTGAGCTTCGCC 659
Db 481 CCAGAGGCGTGC CGGCCAGCGCGGGGGCGGCGAGTGCAACAGAGGGGCTGAGCTTCGCC 540

Qy 660 TGTGATATCTACATCTGGGGCGCTTGGCGGGGACTTGTGGGTCTTCTCTGTGCTG 719
Db 541 TGTGATATCTACATCTGGGGCGCTTGGCGGGGACTTGTGGGTCTTCTCTGTGCTG 600

Qy 720 GTTATCACCTTTTACTGCAACCAACAGGAACCGAAGCGTGTGCAAAATGTCGCCGCGCT 779
Db 601 GTTATCACCTTTTACTGCAACCAACAGGAACCGAAGCGTGTGCAAAATGTCGCCGCGCT 660

Qy 780 GTGTGCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATAGCTCTAA 827
Db 661 GTGTGCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATAGCTCTAA 708
```

RESULT 12
US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.

```
; APPLICANT: Carboni, Joan M.  
; APPLICANT: Rowley, Ronald B.  
; APPLICANT: Wong, Tai W.  
; APPLICANT: Lee, Francis Y.  
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED  
; FILE REFERENCE: D0254 NP  
; CURRENT APPLICATION NUMBER: US/10/378,393  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,889  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 692  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-378-393-2
```

```
Query Match      30.6%; Score 692; DB 7; Length 692;  
Best Local Similarity 100.0%; Pred. No. 9.9e-102;  
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 85 AGCTTCGAGCCCAAGCAGCGTCTCGGGAGCGGTCATGGCCTTACCAGTGAACCGCTTGC 144  
Db 1 AGCTTCGAGCCCAAGCAGCGTCTCGGGAGCGGTCATGGCCTTACCAGTGAACCGCTTGC 60  
Qy 145 TCCTGCGCTGGCTTGTCTCCACGCGCGAGCGAGCGAGTTCGCGGTGTGCGCGC 204  
Db 61 TCCTGCGCTGGCTTGTCTCCACGCGCGAGCGAGCGAGTTCGCGGTGTGCGCGC 120  
Qy 205 TGGATCGGACCTGGAACCTGGGGGAGACAGTGGAGCTGAAGTGCAGGTGTCTGTCCA 264  
Db 121 TGGATCGGACCTGGAACCTGGGGGAGACAGTGGAGCTGAAGTGCAGGTGTCTGTCCA 180  
Qy 265 ACCGAGCTCGGGTGTCTGCTGCTTCCAGCGCGCGCGCGCGCTGAGTCCACCT 324  
Db 181 ACCGAGCTCGGGTGTCTGCTGCTTCCAGCGCGCGCGCGCGCTGAGTCCACCT 240  
Qy 325 TCCTCTATATCTCTCCCAAACCAAGCCAAAGCGCGCGAGGGGTGGACACCCAGCGGT 384  
Db 241 TCCTCTATATCTCTCCCAAACCAAGCCAAAGCGCGCGAGGGGTGGACACCCAGCGGT 300  
Qy 385 TCTCGGCAAGAGGTGGGGGACACTTCTGCTCTCACCCTGAGGACCTTCGCGCGAGAGA 444  
Db 301 TCTCGGCAAGAGGTGGGGGACACTTCTGCTCTCACCCTGAGGACCTTCGCGCGAGAGA 360  
Qy 445 ACAGGGGTACTATTTCTGCTCGGCCCTGAGCAACTCCATCATGTACTTTCAGCCACTTCG 504  
Db 361 ACAGGGGTACTATTTCTGCTCGGCCCTGAGCAACTCCATCATGTACTTTCAGCCACTTCG 420  
Qy 505 TGCGCGTCTTCTGCGCAGCGAAGCCCAACAGACGCGCGCGCGCGAGCCACCAACACCGG 564  
Db 421 TGCGCGTCTTCTGCGCAGCGAAGCCCAACAGACGCGCGCGCGAGCCACCAACACCGG 480  
Qy 565 CGCCCAACATCGGTGCGAGCCCTTGTCTCTGCGCCGAGAGCGGTGCGCGCGAGCGCGG 624  
Db 481 CGCCCAACATCGGTGCGAGCCCTTGTCTCTGCGCCGAGAGCGGTGCGCGCGAGCGCGG 540  
Qy 625 GGGGCGAGTGCAACAGAGGGGTGGACTTTCGCTGTGATATCTACATCTGGGCGCCCT 684  
Db 541 GGGGCGAGTGCAACAGAGGGGTGGACTTTCGCTGTGATATCTACATCTGGGCGCCCT 600  
Qy 685 TGGCGGAGCTTGTGGGTCTCTTCTCTGTCACTGGTTATCACTCCCTTATCACTCAACACA 744  
Db 601 TGGCGGAGCTTGTGGGTCTCTTCTCTGTCACTGGTTATCACTCCCTTATCACTCAACACA 660  
Qy 745 GGAACCGAAGAGCTGTTTGCAAAATGTCGCCG 776  
Db 661 GGAACCGAAGAGCTGTTTGCAAAATGTCGCCG 692
```

RESULT 13

US-10-378-393-6
; Sequence 6, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-6

Query Match 30.6%; Score 692; DB 7; Length 1995;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCTATGCCCTTACCGAGCGCGCTTGC 144
DB 18 AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCTATGCCCTTACCGAGCGCGCTTGC 77
QY 145 TCCTGCCGTGGCCCTTGCTCTCCACGCCGCCAGGCCAGCGAGTTCGGGGTGTGCCCGC 204
DB 78 TCCTGCCGTGGCCCTTGCTCTCCACGCCGCCAGGCCAGCGAGTTCGGGGTGTGCCCGC 137
QY 205 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 264
DB 138 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 197
QY 265 ACCGACGTCGGGCTGCTGGTCTTCCACGCCGCCAGGCCAGCGCGCGCGCGCGCACT 324
DB 198 ACCGACGTCGGGCTGCTGGTCTTCCACGCCGCCAGGCCAGCGCGCGCGCGCACT 257
QY 325 TCCTCTATACCTCTCCCAAAACAAGCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCT 384
DB 258 TCCTCTATACCTCTCCCAAAACAAGCCGAGCGCGCGCGCGCGCGCGCGCGCGCT 317
QY 385 TCTCGGGCAAGAGTTGGGGGACACTTTCGTCCTCACCTGAGCGACTTCCGCGGAGAGA 444
DB 318 TCTCGGGCAAGAGTTGGGGGACACTTTCGTCCTCACCTGAGCGACTTCCGCGGAGAGA 377
QY 445 ACGAGGGTACTATTTTCTCGGCGCTGAGCACTTCATCATGTACTTACGCCACTTGC 504
DB 378 ACGAGGGTACTATTTTCTCGGCGCTGAGCACTTCATCATGTACTTACGCCACTTGC 437
QY 505 TGCCGGTCTTCTGCGAGCGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
DB 438 TGCCGGTCTTCTGCGAGCGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 565 GCCTCACCATCGCGTGCAGCGCCCTGTCTCTGCGCCAGAGCGGTGCCGCGCGCGCG 624
DB 498 GCCTCACCATCGCGTGCAGCGCCCTGTCTCTGCGCCAGAGCGGTGCCGCGCGCGCG 557
QY 625 GGGGCGAGTGCACACGAGGGGCTGGACTTCGCCCTGTGATATCTACATCTGGGGCGCT 684
DB 558 GGGGCGAGTGCACACGAGGGGCTGGACTTCGCCCTGTGATATCTACATCTGGGGCGCT 617
QY 685 TGGCGGAGCTTGTGGGGTCTTCTCTGCTGCTACTGTTATCACCTTACTTGCACACCA 744
DB 618 TGGCGGAGCTTGTGGGGTCTTCTCTGCTGCTACTGTTATCACCTTACTTGCACACCA 677
QY 745 GGAACCGAAGACGTGTTTGCAAATGTCCCCCG 776

DB 678 GGAACCGAAGACGTGTTTGCAAATGTCCCCCG 709

RESULT 14
US-10-378-393-12
; Sequence 12, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-12

Query Match 30.5%; Score 690; DB 7; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCTATGCCCTTACCGAGCGCGCTTGC 144
DB 1 AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCTATGCCCTTACCGAGCGCGCTTGC 60
QY 145 TCCTGCCGTGGCCCTTGCTCTCCACGCCGCCAGGCCAGCGAGTTCGGGGTGTGCCCGC 204
DB 61 TCCTGCCGTGGCCCTTGCTCTCCACGCCGCCAGGCCAGCGAGTTCGGGGTGTGCCCGC 120
QY 205 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 264
DB 121 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 180
QY 265 ACCGACGTCGGGCTGCTGGTCTTCCACGCCGCCAGGCCAGCGCGCGCGCGCGCACT 324
DB 181 ACCGACGTCGGGCTGCTGGTCTTCCACGCCGCCAGGCCAGCGCGCGCGCGCACT 240
QY 325 TCCTCTATACCTCTCCCAAAACAAGCCGAGCGCGCGCGCGCGCGCGCGCGCGCT 384
DB 241 TCCTCTATACCTCTCCCAAAACAAGCCGAGCGCGCGCGCGCGCGCGCGCGCT 300
QY 385 TCTCGGGCAAGAGTTGGGGGACACTTTCGTCCTCACCTGAGCGACTTCCGCGGAGAGA 444
DB 301 TCTCGGGCAAGAGTTGGGGGAGACTTTCGTCCTCACCTGAGCGACTTCCGCGGAGAGA 360
QY 445 ACGAGGGTACTATTTTCTCGGCGCTGAGCACTTCATCATGTACTTACGCCACTTGC 504
DB 361 ACGAGGGTACTATTTTCTCGGCGCTGAGCACTTCATCATGTACTTACGCCACTTGC 420
QY 505 TGCCGGTCTTCTGCGAGCGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
DB 421 TGCCGGTCTTCTGCGAGCGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 565 GCCTCACCATCGCGTGCAGCGCCCTGTCTCTGCGCCAGAGCGGTGCCGCGCGCGCG 624
DB 481 GCCTCACCATCGCGTGCAGCGCCCTGTCTCTGCGCCAGAGCGGTGCCGCGCGCGCG 540
QY 625 GGGGCGAGTGCACACGAGGGGCTGGACTTCGCCCTGTGATATCTACATCTGGGGCGCT 684
DB 541 GGGGCGAGTGCACACGAGGGGCTGGACTTCGCCCTGTGATATCTACATCTGGGGCGCT 600

| | | | |
|----|-----|--|-----|
| Qy | 585 | TGGCCGGGACTTGTGGGGTCCTTCTCCGTGCTACTGGTTATCAACCTTTTACTGCAACCACA | 744 |
| Db | 601 | TGGCCGGGACTTGTGGGGTCCTTCTCCGTGCTACTGGTTATCAACCTTTTACTGCAACCACA | 660 |
| Qy | 745 | GGAAACCGAAGACGTGTTTGCAAATGTCGCC | 774 |
| Db | 661 | GGAAACCGAAGACGTGTTTGCAAATGTCGCC | 690 |

RESULT 15
US-10-378-393-10
; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

| | | | | |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match | 30.5% | Score 690; | DB 7; | Length 2411; |
| Best Local Similarity | 100.0% | Pred. No. 3.1e-101; | | |
| Matches 690; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 85 | AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGCGTCATGGCCCTTACCAGTGACCGCCTTGC | 144 | |
| Db | 1 | AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGCGTCATGGCCCTTACCAGTGACCGCCTTGC | 60 | |
| Qy | 145 | TCCTGCCGTGGCCTTGTGTCTCAACGCCGACAGCCAGTTCGGGTGTGCGCGC | 204 | |
| Db | 61 | TCCTGCCGTGGCCTTGTGTCTCAACGCCGACAGCCAGTTCGGGTGTGCGCGC | 120 | |
| Qy | 205 | TGGATCGGACCTGGAACTCTGGCGGACAGTGGAGCTGAACTGCCAGTGTCTGTGTCCA | 264 | |
| Db | 121 | TGSATCGGACCTGGAACTCTGGCGGACAGTGGAGCTGAACTGCCAGTGTCTGTGTCCA | 180 | |
| Qy | 265 | ACCCGAGCTCGGGTGTCTGTGGCTTCTTCAGCGCGCGCGCGCGCCAGTCCCACT | 324 | |
| Db | 181 | ACCCGAGCTCGGGTGTCTGTGGCTTCTTCAGCGCGCGCGCGCGCCAGTCCCACT | 240 | |
| Qy | 325 | TCCTCTCTATACCTCTCCCAAACCAAGCGCGCGCGAGGGGTGACACCCAGCGGT | 384 | |
| Db | 241 | TCCTCTCTATACCTCTCCCAAACCAAGCGCGCGCGAGGGGTGACACCCAGCGGT | 300 | |
| Qy | 385 | TCTCGGCAAGAGGTGGGGACACCTTCGTCTCTCACCTGAGGACTTCGCCGAGAGA | 444 | |
| Db | 301 | TCTCGGCAAGAGGTGGGGACACCTTCGTCTCTCACCTGAGGACTTCGCCGAGAGA | 360 | |
| Qy | 445 | ACGAGGGCTACTATTCTCTCGCCCTTGAGCACTCCATCATGTACTTCAGCCACTTCG | 504 | |
| Db | 361 | ACGAGGGCTACTATTCTCTCGCCCTTGAGCACTCCATCATGTACTTCAGCCACTTCG | 420 | |
| Qy | 505 | TGCCGTCTTCTGTCCAGCGAAGCCACACAGACGCCAGCGCGCGGACACCAACACCGG | 564 | |
| Db | 421 | TGCCGTCTTCTGTCCAGCGAAGCCACACAGACGCCAGCGCGCGGACACCAACACCGG | 480 | |
| Qy | 565 | CGCCCAACATCGCGTCGAGCCCTGTCTCTTCGCCCCAGAGCGGTGCCGCCAGCGCGG | 624 | |
| Db | 481 | CGCCCAACATCGCGTCGAGCCCTGTCTCTTCGCCCCAGAGCGGTGCCGCCAGCGCGG | 540 | |

| Result No. | Query | | | DB | ID | Description |
|------------|-------|-------|--------|----|---------------------|--------------------|
| | Score | Match | Length | | | |
| 1 | 2261 | 100.0 | 2261 | 6 | US-10-511-937-415 | Sequence 415, Appl |
| 2 | 134.6 | 5.8 | 1999 | 6 | US-10-505-928-758 | Sequence 758, Appl |
| 3 | 131 | 5.8 | 2040 | 6 | US-10-953-349-37996 | Sequence 37996, A |
| 4 | 130.6 | 5.8 | 4670 | 7 | US-11-145-307A-29 | Sequence 29, Appl |
| 5 | 129.4 | 5.7 | 2846 | 6 | US-10-196-749-169 | Sequence 169, Appl |
| 6 | 129.4 | 5.7 | 2846 | 7 | US-11-101-316-37 | Sequence 37, Appl |
| 7 | 128.4 | 5.7 | 2442 | 6 | US-10-953-349-35802 | Sequence 35802, A |
| 8 | 126 | 5.6 | 1985 | 6 | US-10-196-749-27 | Sequence 27, Appl |
| 9 | 126 | 5.6 | 2773 | 6 | US-10-196-749-149 | Sequence 149, Appl |
| 10 | 126 | 5.6 | 2773 | 7 | US-11-101-316-33 | Sequence 33, Appl |
| 11 | 121.6 | 5.4 | 2272 | 6 | US-10-953-349-37381 | Sequence 37381, A |
| 12 | 117.8 | 5.2 | 2861 | 6 | US-10-953-349-7328 | Sequence 7328, Ap |
| 13 | 116.8 | 5.2 | 2163 | 6 | US-10-953-349-37514 | Sequence 37514, A |
| 14 | 115.8 | 5.1 | 1843 | 6 | US-10-511-937-620 | Sequence 620, Appl |
| 15 | 115.2 | 5.1 | 2205 | 6 | US-10-953-349-9921 | Sequence 9921, Ap |
| 16 | 114.4 | 5.1 | 641 | 6 | US-10-488-619-1577 | Sequence 1577, Ap |
| 17 | 114 | 5.0 | 4640 | 6 | US-10-196-749-75 | Sequence 75, Appl |
| 18 | 113.8 | 5.0 | 1734 | 6 | US-10-196-749-201 | Sequence 201, Appl |
| 19 | 113.8 | 5.0 | 1734 | 7 | US-11-101-316-51 | Sequence 51, Appl |
| 20 | 113.4 | 5.0 | 1292 | 6 | US-10-953-349-10307 | Sequence 10307, A |
| 21 | 111.4 | 4.9 | 1771 | 6 | US-10-196-749-17 | Sequence 17, Appl |
| 22 | 111.4 | 4.9 | 1771 | 7 | US-11-296-092-36 | Sequence 36, Appl |
| 23 | 109 | 4.8 | 1837 | 6 | US-10-511-937-537 | Sequence 537, Appl |
| 24 | 109 | 4.8 | 1837 | 6 | US-10-516-478-7 | Sequence 7, Appl |
| 25 | 108.4 | 4.8 | 1528 | 6 | US-10-953-349-28506 | Sequence 28506, A |

QY 181 CGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
QY 241 TGAAGTGCAGGTGCTGTCGTCGAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
Db 241 TGAAGTGCAGGTGCTGTCGTCGAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
QY 301 CGCGCGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
Db 301 CGCGCGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
QY 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
Db 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGGACACCTTCTGCTCTCA 420
QY 421 CCCTGAGCGACTTCCGCGAGAGAACAGGAGGCTACTATTCTGCTCGGCCCTGAGCAACT 480
Db 421 CCCTGAGCGACTTCCGCGAGAGAACAGGAGGCTACTATTCTGCTCGGCCCTGAGCAACT 480
QY 481 CCATCATGTACTTCAGCCACTTCTGTCGGGCTTCTCCGACGAAAGCCACACGACGC 540
Db 481 CCATCATGTACTTCAGCCACTTCTGTCGGGCTTCTCCGACGAAAGCCACACGACGC 540
QY 541 CAGCGCCGACCAACACACGCGGCCCAACCATCGCTCGAGGCCCTGTCCCTGCGCC 600
Db 541 CAGCGCCGACCAACACACGCGGCCCAACCATCGCTCGAGGCCCTGTCCCTGCGCC 600
QY 601 CAGAGGCGTCCGCGACGCGGCGGCGCAGTGCACACGAGGGGCTGACCTTCGCGCT 660
Db 601 CAGAGGCGTCCGCGACGCGGCGGCGCAGTGCACACGAGGGGCTGACCTTCGCGCT 660
QY 661 GTGATATCTACATCTGGGCGCCCTTGGCGGAGCTTGTGGGTCCTTCTCTGTCACCTGG 720
Db 661 GTGATATCTACATCTGGGCGCCCTTGGCGGAGCTTGTGGGTCCTTCTCTGTCACCTGG 720
QY 721 TTATCACCCTTTACTGCAACCAACAGGACCGGAGAGCTGTTTGCAGGCTCCCGGCGCTG 780
Db 721 TTATCACCCTTTACTGCAACCAACAGGACCGGAGAGCTGTTTGCAGGCTCCCGGCGCTG 780
QY 781 TGGTCAAAATCGGAGACAGCCAGCTTTTGGCGAGATACGCTTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAGCCAGCTTTTGGCGAGATACGCTTAAACCTGTGCAACAG 840
QY 841 CCATCATATTACTTCAAACTGAGATCTTCTCTTTTGGGAGCAAGTCTTCCCTTTCAT 900
Db 841 CCATCATATTACTTCAAACTGAGATCTTCTCTTTTGGGAGCAAGTCTTCCCTTTCAT 900
QY 901 TTTTTCAGTCTTCTCCTGTGATTCATCTCATGATTAATTTTAGTGGGGCGGG 960
Db 901 TTTTTCAGTCTTCTCCTGTGATTCATCTCATGATTAATTTTAGTGGGGCGGG 960
QY 961 GTGGAAAGATTACTTTTTTTTATGTTTTCAGCGGAAACAAACTAGGTAAATCTAC 1020
Db 961 GTGGAAAGATTACTTTTTTTTATGTTTTCAGCGGAAACAAACTAGGTAAATCTAC 1020
QY 1021 AGTACACCAAGGGTCAATPACTGTTGTGCGCACATCGCGGTAGGCGTGAAGGGG 1080
Db 1021 AGTACACCAAGGGTCAATPACTGTTGTGCGCACATCGCGGTAGGCGTGAAGGGG 1080
QY 1081 CAGGCGAGAGTACCGGAGAGTTCTCAGAAATCATGCTGAGAGCTGGAGGCCCATG 1140
Db 1081 CAGGCGAGAGTACCGGAGAGTTCTCAGAAATCATGCTGAGAGCTGGAGGCCCATG 1140
QY 1141 CCATCTCAACCTTCTCCCGCCGTTTACAAAGGGGAGGCTAAAGCCAGAGCAGCT 1200
Db 1141 CCATCTCAACCTTCTCCCGCCGTTTACAAAGGGGAGGCTAAAGCCAGAGCAGCT 1200
QY 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTACGTGAGGACCTTGTCTCCA 1260
Db 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTACGTGAGGACCTTGTCTCCA 1260
QY 1261 GCTCAGGGCTCTTCTCTCCACACCATTCAGGCTCTTCTTCCGAGGCCCTGCTCAGGG 1320

Db 1261 GCTCAGGGCTCTTCTCTCCACCATTCAGGCTCTTCTTCCGAGGCCCTGCTCAGGG 1320
QY 1321 TGAGGTGCTTGGTCTCCACGCAAGGAAACAAAGTACTTCTTGTATACCTGGGATACTGT 1380
Db 1321 TGAGGTGCTTGGTCTCCACGCAAGGAAACAAAGTACTTCTTGTATACCTGGGATACTGT 1380
QY 1381 GCCCAGAGCTTCGAGGAGGTAATGAATTAAGAGAGAACTGCTTTCGGCAGAGTTCTAT 1440
Db 1381 GCCCAGAGCTTCGAGGAGGTAATGAATTAAGAGAGAACTGCTTTCGGCAGAGTTCTAT 1440
QY 1441 AATCTTAAACAATATCAGACTTTTTTTTTTATATCAAGCCCTAAATTTGTATAGACCTAA 1500
Db 1441 AATCTTAAACAATATCAGACTTTTTTTTTTATATCAAGCCCTAAATTTGTATAGACCTAA 1500
QY 1501 AATAAAATGAAGTGGTGAAGCTTAAACCCCTGGAAAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 1501 AATAAAATGAAGTGGTGAAGCTTAAACCCCTGGAAAAATGAATCCCTCTATCTCTAAAGAAAT 1560
QY 1561 CTCTGTGAAACCCCTATGTGGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCGAGAGGG 1620
Db 1561 CTCTGTGAAACCCCTATGTGGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCGAGAGGG 1620
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
QY 1681 CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGGATCAGTGATGA 1740
Db 1681 CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGGATCAGTGATGA 1740
QY 1741 CTTTTTATATCTTTGTAAGACAAATTTTGGAGAGCCCTCACAAGCCCTGSCCTCTGCT 1800
Db 1741 CTTTTTATATCTTTGTAAGACAAATTTTGGAGAGCCCTCACAAGCCCTGSCCTCTGCT 1800
QY 1801 CAATAGCAGATACAGGGATCAGGACCTGACCTCTCTTAAAGGAGGCTGAGAGCCCAAA 1860
Db 1801 CAATAGCAGATACAGGGATCAGGAGGACCTGACCTCTCTTAAAGGAGGCTGAGAGCCCAAA 1860
QY 1861 CTGCTGTCCCAACATGCACTTCTCTTAAAGGTATGTTCAAGCAATGCTGCCCATTT 1920
Db 1861 CTGCTGTCCCAACATGCACTTCTCTTAAAGGTATGTTCAAGCAATGCTGCCCATTT 1920
QY 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTTACCTTAGG 1980
Db 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTTACCTTAGG 1980
QY 1981 AATAATCTCTGTTAATAATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATAATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
QY 2041 AATATGCTTTCTTTTAAATAGGGTTGATGCTATGCTTATGATGCTTTAATGAAT 2100
Db 2041 AATATGCTTTCTTTTAAATAGGGTTGATGCTATGCTTATGATGCTTTAATGAAT 2100
QY 2101 AAAACATTTGTAGCATCTCTTTAATGAGTAAACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2160
Db 2101 AAAACATTTGTAGCATCTCTTTAATGAGTAAACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2160
QY 2161 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
Db 2161 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
QY 2221 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2281
Db 2221 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2281

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; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 758
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-758

Query Match          6.0%; Score 134.6; DB 6; Length 1999;
Best Local Similarity 70.8%; Pred. No. 4.2e-11;
Matches 179; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2009 TCTTCTCGATTATTTCTACACATACATGTAATAATATGCTTTCTTTTAAATAGGGTT 2068
Dbb 1724 TTTTGTAGAGAAATTAGAACCCATACACATGCTATCAACATGTTATTCAATGG 1783
QY 2069 GTACTATGCTGTATGAGTGGCTTTAATGAATAAATTTGTAGCATCTCTTTAATGGG 2128
Dbb 1784 ACACCTAACTCTTTTCTATTATTTTAAAGTAAAGACTTTTATTAAATAAAACAAATGT 1843
QY 2129 TAAACAGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2188
Dbb 1844 TTTGAGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1903
QY 2189 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2248
Dbb 1904 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1963
QY 2249 AAAAAAATAAAAAA 2261
Dbb 1964 AAAAAAATAAAAAA 1976

RESULT 3
US-10-953-349-37996
; Sequence 37996, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37996
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37996

Query Match          5.8%; Score 131; DB 6; Length 2040;
Best Local Similarity 87.7%; Pred. No. 1.3e-10;
Matches 143; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2099 ATAACATTGTGACATCTCTTTAATGGTTAAACAGCAAAAAAATAAAAAAATAAAAAA 2158
Dbb 1730 AGATAAGTTTGTAGTTGATTATATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1789
QY 2159 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2218
Dbb 1790 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1849
QY 2219 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2261
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Dbb 1850 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1892

RESULT 4
US-11-145-307A-29
; Sequence 29, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 4670
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-29

Query Match          5.8%; Score 130.6; DB 7; Length 4670;
Best Local Similarity 83.6%; Pred. No. 1.5e-10;
Matches 148; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 2076 GCTGTATGAGTGGCTTTAATGAATAAACAATTTGTAGCATCTCTTTAATGGTAAACAG 2135
Dbb 4494 GCTTTTGTGGGGTTTTTATTTTAAAGAAACACTCAATCATCTCTAAAAAATAAAAAA 4553
QY 2136 CAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2195
Dbb 4554 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4613
QY 2196 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2252
Dbb 4614 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4670

RESULT 5
US-10-196-749-169
; Sequence 169, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
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; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 169
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-169

Query Match 5.7%; Score 129.4; DB 6; Length 2846;
Best Local Similarity 84.8%; Pred. No. 2.1e-10; Mismatches 26; Indels 0; Gaps 0;
Matches 145; Conservative 0;

Qy 2091 TTTAATGAATAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2150
Db 2668 TCTCTGTACACATTTAATAAATAAGGGTTGGCTTCTGAACTACAAAAA 2727

Qy 2151 AAAAAA 2210
Db 2728 AAAAAA 2787

Qy 2211 AAAAAA 2261
Db 2788 AAAAAA 2838

RESULT 6
US-11-101-316-37
; Sequence 37, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Auscin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/066867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 37
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-37

Query Match 5.7%; Score 129.4; DB 7; Length 2846;
Best Local Similarity 84.8%; Pred. No. 2.1e-10;
Matches 145; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2091 TTTAATGAATAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2150
Db 2668 TCTCTGTACACATTTAATAAATAAGGGTTGGCTTCTGAACTACAAAAA 2727

Qy 2151 AAAAAA 2210
Db 2728 AAAAAA 2787

Qy 2211 AAAAAA 2261
Db 2788 AAAAAA 2838

RESULT 7
US-10-953-349-35802
; Sequence 35802, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35802
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (539)..(539)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (659)..(660)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2409)..(2411)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2432)..(2433)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35802

Query Match 5.7%; Score 128.4; DB 6; Length 2442;
Best Local Similarity 87.0%; Pred. No. 2.9e-10; Mismatches 21; Indels 0; Gaps 0;
Matches 141; Conservative 0;

Qy 2100 TAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2159
Db 2211 TACATACCCGAAGGTTGTCCTTGACATAAAAA 2270

Qy 2160 AAAAAA 2219
Db 2271 AAAAAA 2330

Qy 2220 AAAAAA 2261
Db 2331 AAAAAA 2372

RESULT 8
US-10-196-749-27
; Sequence 27, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc


```

; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 27
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-27

Query Match 5.6%; Score 126; DB 6; Length 1985;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 2136 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Db 1958 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Qy 2196 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Db 1918 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Qy 2256 AAAAAA 2261
Db 1978 AAAAAA 1983

RESULT 9
US-10-196-749-149
; Sequence 149, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 33
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-33

Query Match 5.6%; Score 126; DB 7; Length 2773;
Best Local Similarity 93.0%; Pred. No. 6.1e-10;
Matches 132; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 2120 TTTAATGGGTAAACAGCAA 2179
Db 2631 TTTAATGGTGTAGAGGATCAAAATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2690
Qy 2180 AA 2239
Db 2691 AA 2750
Qy 2240 AAAAAAAAAAAAAAAAAAAAAA 2261
Db 2751 AAAAAAAAAAAAAAAAAAAAAA 2772

RESULT 11
US-10-953-349-37381
; Sequence 37381, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37381
; LENGTH: 2272
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (2086)..(2086)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-37381

Query Match 5.4%; Score 121.6; DB 6; Length 2272;
Best Local Similarity 80.2%; Pred. No. 2.4e-09;
Matches 142; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
Qy 2085 AGTGCCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAA 2144
Db 2019 ACTGAGTTACAGCAGAGATGAATTTCTCGATCCTAAATGCAGAGATTAATAATAAATAA 2078
Qy 2145 AA 2204
Db 2079 TATATAAAGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2138
Qy 2205 AA 2261
Db 2139 AA 2195

RESULT 12
US-10-953-349-7328
; Sequence 7328, Application US/10953349
; Publication No. US20060107345A1

; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7328
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7328

Query Match 5.2%; Score 117.8; DB 6; Length 2861;
Best Local Similarity 66.1%; Pred. No. 7.9e-09;
Matches 170; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
Qy 1997 TATGGGTGACATTTCTTCTCGATTAATTTTCTACATACATGTAATAATATGCTTTCTTTT 2056
Db 1502 TTTGGCTCCCTTGTGGATGATGTTGGTATATGATGTATATGATGTATATACAGAGGCTCTATG 1561
Qy 2057 TTTAATAGGGTTGACTATGCTGTTATCAGTGGCTTTAATGAATAAACATTTGTAGCATC 2116
Db 1562 TAAATAACGTTTCTCGTTTTTTTATCAGTGAATCACTTATTTCTTTTCTTTAACAATG 1621
Qy 2117 CTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2176
Db 1622 TCGATTTGTAATAGATTCATGTGTTCAACAAAAAATAAAAAAAAAAAAAAAAAAAAAA 1681
Qy 2177 AA 2236
Db 1682 AA 1741
Qy 2237 AAAAAAAAAAAAAAAAAAAAAA 2253
Db 1742 AAAAAAAAAAAAAAAGA 1758

RESULT 13
US-10-953-349-37514
; Sequence 37514, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37514
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37514

Query Match 5.2%; Score 116.8; DB 6; Length 2163;
Best Local Similarity 88.2%; Pred. No. 1.1e-08;
Matches 127; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 2110 TAGCATCTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2169
Db 1956 TATGAATCAGTTTGTCTGATTTTTCATAAAAAAAAAAAAAAGAAAAAAAAAAAAA 2015
Qy 2170 AA 2229
Db 2016 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2075
Qy 2230 AAAAAAAAAAAAAAAAAAAAAA 2253

Db 2076 AAAAAAAAAAAAAAAAAAAAAA 2099

RESULT 14

US-10-511-937-620
; Sequence 620, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 620
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-620

Query Match 5.1%; Score 115.8; DB 6; Length 1843;
Best Local Similarity 94.5%; Pred. No. 1.4e-08;
Matches 120; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2135 GCATTAAGTAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2194
Db 1709 GCTTAAGTAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1768

QY 2195 AA 2254
Db 1769 AA 1828

QY 2255 AAAAAAA 2261
Db 1829 AAAAAAA 1835

RESULT 15
US-10-953-349-9921
; Sequence 9921, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9921
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9921

Query Match 5.1%; Score 115.2; DB 6; Length 2205;
Best Local Similarity 87.5%; Pred. No. 1.7e-08;

Matches 126; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2118 TCTTTAATCGGTAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2177
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QY 2178 AA 2237
Db 2050 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 2109

QY 2238 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db 2110 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133

Search completed: May 30, 2006, 04:09:53
Job time : 68 secs

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: May 30, 2006, 03:27:54 ; Search time 9648 Seconds
(without alignments)
13104.644 Million cell updates/sec
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Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
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12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | |
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| 1 | 1827 | 80.8 | CR619549 full-length |
| 2 | 881.8 | 33.0 | AL575755 |
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| 4 | 785.6 | 34.8 | 882 2 BI820267 |
| 5 | 775.4 | 34.3 | 789 2 BI819839 |
| 6 | 764.8 | 33.8 | 838 9 DA931234 |
| 7 | 763.4 | 33.8 | 847 4 BX437211 |
| 8 | 744.8 | 32.9 | 804 2 BI820808 |
| 9 | 724.4 | 32.0 | 780 2 BI760947 |
| 10 | 708 | 31.3 | 749 7 AW949684 |
| 11 | 705.8 | 31.2 | 796 2 BI911195 |
| 12 | 703.4 | 31.1 | 949 8 CO646993 |
| 13 | 697 | 30.8 | 704 9 DN997301 |
| 14 | 692.6 | 30.6 | 744 7 AW006735 |
| 15 | 678.4 | 30.0 | 884 1 AL552456 |
| 16 | 676 | 29.9 | 727 1 AI992204 |
| 17 | 674.4 | 29.8 | 768 2 BI820031 |
| 18 | 654 | 28.9 | 1109 4 BX415859 |
| 19 | 627 | 27.7 | 9 627 9 DA371487 |

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| 20 | 626 | 27.7 | 628 | 9 | DB123661 |
| 21 | 625.2 | 27.7 | 757 | 5 | CD638588 |
| 22 | 618.4 | 27.4 | 620 | 9 | DA381496 |
| 23 | 617 | 27.3 | 1024 | 4 | EX327291 |
| 24 | 612.2 | 27.1 | 755 | 9 | DR007174 |
| 25 | 611 | 27.0 | 611 | 9 | DB123733 |
| 26 | 603.4 | 26.7 | 840 | 2 | BI835165 |
| 27 | 602.4 | 26.6 | 604 | 9 | DB123560 |
| 28 | 600.2 | 26.5 | 708 | 4 | CB552318 |
| 29 | 600 | 26.5 | 600 | 9 | DB117237 |
| 30 | 599 | 26.5 | 599 | 9 | DA938336 |
| 31 | 598.4 | 26.5 | 619 | 7 | BE646138 |
| 32 | 597.4 | 26.4 | 599 | 9 | DA935416 |
| 33 | 597 | 26.4 | 597 | 9 | DA940156 |
| 34 | 596 | 26.4 | 598 | 9 | DA936524 |
| 35 | 595 | 26.3 | 595 | 9 | DA935186 |
| 36 | 594 | 26.3 | 594 | 2 | BI760884 |
| 37 | 593.4 | 26.2 | 596 | 9 | DA940758 |
| 38 | 593 | 26.2 | 593 | 9 | DA421985 |
| 39 | 593 | 26.2 | 593 | 9 | DB110805 |
| 40 | 592.6 | 26.2 | 661 | 4 | CB553966 |
| 41 | 592.4 | 26.2 | 606 | 9 | DA936371 |
| 42 | 592 | 26.2 | 592 | 9 | DA670538 |
| 43 | 590 | 26.1 | 602 | 9 | DB110509 |
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| 45 | 588 | 26.0 | 635 | 9 | DA377933 |

ALIGNMENTS

CR619549 1948 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CSODI070YG17 of Placenta Cot 25-normalized
of Homo sapiens (human).
CR619549
CR619549.1 GI:50500356
HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1948)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1948)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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Query Match 80.8%; Score 1827; DB 6; Length 1948;

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| Best Local Similarity 94.6%; Pred. No. 0; | | | |
| Matches 1948; Conservative 0; Mismatches 0; Indels 111; Gaps 1; | | | |
| Qy | 50 | CCCCACGGCTCCCGCGGCTCCCTCGCGCCCGAGCTTCAGCAAGCAGCGTCTGG | 109 |
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| Qy | 110 | GGAGCGGTATGCGCTTACAGTGACCGCTTCTCGCGCTGGCTTGTCTGCTCA | 169 |
| Db | 61 | GGAGCGGTATGCGCTTACAGTGACCGCTTCTCGCGCTGGCTTGTCTGCTCA | 120 |
| Qy | 170 | CGCGCCAGGCGGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGGGGA | 229 |
| Db | 121 | CGCGCCAGGCGGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGGGGA | 180 |
| Qy | 230 | GACAGTGAGCTGAAGTGCAGGTGCTGTCCAAACCGAGCTCGGCTCTCGTGGCT | 289 |
| Db | 181 | GACAGTGAGCTGAAGTGCAGGTGCTGTCCAAACCGAGCTCGGCTCTCGTGGCT | 240 |
| Qy | 290 | CTTCCAGCGCGCGCGCGCTTCCAGTCCCACTTCTCTATACCTTCTCCCAAAACA | 349 |
| Db | 241 | CTTCCAGCGCGCGCGCGCTTCCAGTCCCACTTCTCTATACCTTCTCCCAAAACA | 300 |
| Qy | 350 | GCCCAAGCGCGGAGGGCTGGACACCGAGGTTCTCGGCAAGAGTTGGGGACAC | 409 |
| Db | 301 | GCCCAAGCGCGGAGGGCTGGACACCGAGGTTCTCGGCAAGAGTTGGGGACAC | 360 |
| Qy | 410 | CTTGGCTCTACCTGAGCGCTTCCGCGGAGAGAACGAGGCTACTATTCTGCTGGC | 469 |
| Db | 361 | CTTGGCTCTACCTGAGCGCTTCCGCGGAGAGAACGAGGCTACTATTCTGCTGGC | 420 |
| Qy | 470 | CCTGAGCAACTCCATCATGTACTTTCAGCCACTTCTGTCGGTCTTCTCGCAGCAAGCC | 529 |
| Db | 421 | CCTGAGCAACTCCATCATGTACTTTCAGCCACTTCTGTCGGTCTTCTCGCAGCAAGCC | 480 |
| Qy | 530 | CACACGAGCGGCGGCGGACCAACACCGCGCGCCACCATCGCGTCCGAGCCCT | 589 |
| Db | 481 | CACACGAGCGGCGGCGGACCAACACCGCGCGCCACCATCGCGTCCGAGCCCT | 540 |
| Qy | 590 | GTCCCTGCGCCAGAGGGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 649 |
| Db | 541 | GTCCCTGCGCCAGAGGGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 584 |
| Qy | 650 | GGACTTCCCTGTGATATCTATCTGCGCGCGCTTGGCGCGGACTTGTGGGCTCTTCT | 709 |
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| Qy | 710 | CCTGTCACTGGTTATCACCCCTTACTGCAACCAAGGAAACGAGACGTGTTGCAATG | 769 |
| Db | 595 | -----GGAAACCGAAGACGTGTTGCAATG | 609 |
| Qy | 770 | TCCCGGCTGTGGTCAAACTCGGAGACAAGCCAGCCCTTTCGGCGAGATAGCTTAACC | 829 |
| Db | 610 | TCCCGGCTGTGGTCAAACTCGGAGACAAGCCAGCCCTTTCGGCGAGATAGCTTAACC | 669 |
| Qy | 830 | CTGTGCAACAGCACTACATTAATCTTCAAACTGAGTCTCTTCTTGGGAGCAAGTCC | 889 |
| Db | 670 | CTGTGCAACAGCACTACATTAATCTTCAAACTGAGTCTCTTCTTGGGAGCAAGTCC | 729 |
| Qy | 890 | TTCCCTTTCAATTTTCCAGTCTTCTCGCTGTGTATTCATTCATGATTAATTTTA | 949 |
| Db | 730 | TTCCCTTTCAATTTTCCAGTCTTCTCGCTGTGTATTCATTCATGATTAATTTTA | 789 |
| Qy | 950 | GTGGGGGGGGTGGGAAAGATTACTTTTCTTATGTGTTTGAGCGGAAACAAACTAG | 1009 |
| Db | 790 | GTGGGGGGGGTGGGAAAGATTACTTTTCTTATGTGTTTGAGCGGAAACAAACTAG | 849 |
| Qy | 1010 | GTAATACTACAGTACACCAAGGGTCAATACTGTGTGCGCACATCGCGGTAGGCG | 1069 |
| Db | 850 | GTAATACTACAGTACACCAAGGGTCAATACTGTGTGCGCACATCGCGGTAGGCG | 909 |
| Qy | 1070 | GTGGAAGGGCGGAGGCTACCGCAGGTTCTCAGATCATGCTGAGAGCTGG | 1129 |

| | | | |
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| Db | 910 | GTGGAAGGGCGAGGCGCAGAGCTACCCGCAAGTTCCTCAGAAATCATGCTGAGAGCTGG | 969 |
| Qy | 1130 | AGGCACCCATGCCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGAGGCTAAAGCC | 1189 |
| Db | 970 | AGGCACCCATGCCATCTCAACCTCTTCCCGCCCGTTTTTACAAAGGGGAGGCTAAAGCC | 1029 |
| Qy | 1190 | CAGAGACGCTTGATTAAGGCAACAGCAAGTCAAGGTTGGAGGAGTAGCTGAGGGAC | 1249 |
| Db | 1030 | CAGAGACGCTTGATTAAGGCAACAGCAAGTCAAGGTTGGAGGAGTAGCTGAGGGAC | 1089 |
| Qy | 1250 | CTTGTCTCCAGCTCAGGCTCTTCTCCACACCATTCAGGTCTTCTTCCGAGGCC | 1309 |
| Db | 1090 | CTTGTCTCCAGCTCAGGCTCTTCTCCACACCATTCAGGTCTTCTTCCGAGGCC | 1149 |
| Qy | 1310 | CTGTCTCAGGCTGAGGTCTTGTAGTCTCCAAACGCGCAAGGAACTGTAATCTTCTGATACC | 1369 |
| Db | 1150 | CTGTCTCAGGCTGAGGTCTTGTAGTCTCCAAACGCGCAAGGAACTGTAATCTTCTGATACC | 1209 |
| Qy | 1370 | TGGGATCTGTGCGCAGGCTCGAGGAGTAAATTAAGAAAGAGAACTGCCCTTGG | 1429 |
| Db | 1210 | TGGGATCTGTGCGCAGGCTCGAGGAGTAAATTAAGAAAGAGAACTGCCCTTGG | 1269 |
| Qy | 1430 | CAGAGTCTATAATGTAACCAATATCAGCTTTTTTTTTTTTATTAATCAAGCTAAATTTG | 1489 |
| Db | 1270 | CAGAGTCTATAATGTAACCAATATCAGCTTTTTTTTTTTTATTAATCAAGCTAAATTTG | 1329 |
| Qy | 1490 | TATAGACTTAAATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT | 1549 |
| Db | 1330 | TATAGACTTAAATAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT | 1389 |
| Qy | 1550 | CTAAAGAAATCTCTGTGAAACCCCTATGTGGAGCGGAAATGTCTCCAGCCCTTGA | 1609 |
| Db | 1390 | CTAAAGAAATCTCTGTGAAACCCCTATGTGGAGCGGAAATGTCTCCAGCCCTTGA | 1449 |
| Qy | 1610 | TTGAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTTAAATAGAAATTTGAGCATCA | 1669 |
| Db | 1450 | TTGAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTTAAATAGAAATTTGAGCATCA | 1509 |
| Qy | 1670 | GTGAGGTTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTCTGG | 1729 |
| Db | 1510 | GTGAGGTTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTCTGG | 1569 |
| Qy | 1730 | ATCATGATGATCTTTTATATCTTTGTAAGACAATTTGTTGGAGAGCCCTCACAGGCC | 1789 |
| Db | 1570 | ATCATGATGATCTTTTATATCTTTGTAAGACAATTTGTTGGAGAGCCCTCACAGGCC | 1629 |
| Qy | 1790 | TGGCTCTGCTCACTAGCAGATACAGGATGAGGACACCTGACTCTCTTAAAGGAGCT | 1849 |
| Db | 1630 | TGGCTCTGCTCACTAGCAGATACAGGATGAGGACACCTGACTCTCTTAAAGGAGCT | 1689 |
| Qy | 1850 | GAGAGCCCAAACTGCTGTCCCAAAACATGCACTTCTTCTTAAAGTATGTTACAGCAAT | 1909 |
| Db | 1690 | GAGAGCCCAAACTGCTGTCCCAAAACATGCACTTCTTCTTAAAGTATGTTACAGCAAT | 1749 |
| Qy | 1910 | GCCTGCCCATTTGGAGAGAAAACTTAAAGTATGAGGAAATAGAAACCACTATAATTC | 1969 |
| Db | 1750 | GCCTGCCCATTTGGAGAGAAAACTTAAAGTATGAGGAAATAGAAACCACTATAATTC | 1809 |
| Qy | 1970 | TTCACTTTAGGAATACTCTGTTTAAATGTTGATCTTCTGATTTATTTTCTACA | 2029 |
| Db | 1810 | TTCACTTTAGGAATACTCTGTTTAAATGTTGATCTTCTGATTTATTTTCTACA | 1869 |
| Qy | 2030 | CATACATGAAAAATGCTTTTCTTTTAAATAGGGTGTACTATGCTGTTATGAGTGG | 2089 |
| Db | 1870 | CATACATGAAAAATGCTTTTCTTTTAAATAGGGTGTACTATGCTGTTATGAGTGG | 1929 |
| Qy | 2090 | CTTTAATGAATAAATTT 2108 | |
| Db | 1930 | CTTTAATGAATAAATTT 1948 | |

LOCUS AL575755 936 bp mRNA linear EST 06-APR-2004
DEFINITION AL575755 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI070YG17 3-PRIME, mRNA sequence.
ACCESSION AL575755
VERSION AL575755.3 GI:46248682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31314055.
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1670.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DI070AD09NP1&c=1670.r.

FEATURES
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 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 39.0%; Score 881.8; DB 1; Length 936;
 Best Local Similarity 97.1%; Pred. No. 2e-157;
 Matches 909; Conservative 8; Mismatches 16; Indels 3; Gaps 2;

QY 1176 GGGAGCTAAAGCCAGACAGCTTGATCAAGGCACACACAGTCAGGCTCGAGCA 1235
 Db GGGGAGCTAAGCCAGACAGCTTGATCAAGGCACACACAGTCAGGCTCGAGCA 877
 QY 1236 GTAGCTGGAGGACCTTGTCTCCAGCTCAGGCTCTTTCCCTCCACACCATTCAGTCTT 1295
 Db GTAGCTGGAGGACCTTGTCTCCAGCTCAGGCTCTTTCCCTCCACACCATTCAGTCTT 817
 QY 1296 TCTTTCCGAGGCCCTGTCTCAGGCTAGGCTCTTCAAGTCTCAACGGCAAGGCAACAG 1355
 Db TCTTTCCGAGGCCCTGTCTCAGGCTAGGCTCTTCAAGTCTCAACGGCAAGGCAACAG 757
 QY 1356 TACTTCTTGATACCTGGGATCTGTGCCAGAGCTCGAGAGGTAATGAATTAAGAG 1415
 Db TACTTCTTGATACCTGGGATCTGTGCCAGAGCTCGAGAGGTAATGAATTAAGAGAG 697
 QY 1416 AGAAGCTGCTTGGCAGAGTCTTATAATGTAACAATATCAGAC--TTTTTTTTTTATA 1473
 Db AGAAGCTGCTTGGCAGAGTCTTATAATGTAACAATATCAGACCTTTTTTTTTTTATA 637
 QY 1474 ATCAAGCTTAAATTTGTATAGACCTTAAATAAATAAGTGTGAGCTTAAACCTGGAAA 1533
 Db ATCAAGCTTAAATTTGTATAGACCTTAAATAAATAAGTGTGAGCTTAAACCTGGAAA 577
 QY 1534 ATGATCCCTCTATCTTAAGAAAAATCTCTGTGAACCCCTATGTGAGGCGGAATTGC 1593
 Db ATGATCCCTCTATCTTAAGAAAAATCTCTGTGAACCCCTATGTGAGGCGGAATTGC 517

1594 TCTCCAGCCCTTGCAATTCAGAGGGGCCCATGAAAGAGGACAGGCTACCCCTTTACAAA 1653
 Db TCTCCAGCCCTTGCAATTCAGAGGGGCCCATGAAAGAGGACAGGCTACCCCTTTACAAA 457
 QY 1654 TAGAATTTGAGCATCAGTCAGGTTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATA 1713
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 QY 1714 CAAACATGTTCTCGGATCAGTCAGTATTTTATATCTTTTAAAGCAACAATTTGAGATA 1773
 Db CAAACATGTTCTCGGATCAGTCAGTATTTTATATCTTTTAAAGCAACAATTTGAGATA 337
 QY 1774 GCCCTTACACAGCCCTGCGCTCTGCTCAACTAGCAGATACAGGGATGAGGCAGACCTGA 1833
 Db GCCCTTACACAGCCCTGCGCTCTGCTCAACTAGCAGATACAGGGATGAGGCAGACCTGA 277
 QY 1834 CTCTCTTAAGAGGCTGAGAGCCCAAACTGCTGTGCCAAACATGCACTTCCTTGCCTTAAG 1893
 Db CTCTCTTAAGAGGCTGAGAGCCCAAACTGCTGTGCCAAACATGCACTTCCTTGCCTTAAG 217
 QY 1894 GTATGTTACAAGCAATGCTGCCCATTTGGAGAGAAAACTTAAGTAGATAGGAATAA 1953
 Db GTATGTTACAAGCAATGCTGCCCATTTGGAGAGAAAACTTAAGTAGATAGGAATAA 157
 QY 1954 GAACCACTCATATTTCTTCACTTAGGAATAATCTCTGTAAATATGTTGATCATTTCTTC 2013
 Db GAACCACTCATATTTCTTCACTTAGGAATAATCTCTGTAAATATGTTGATCATTTCTTC 97
 QY 2014 CTGATATTTTCTACATACATGATAAATATGTTCTTTTAAATAGGTTGTTACT 2073
 Db CTGATATTTTCTACATACATGATAAATATGTTCTTTTAAATAGGTTGTTACT 37
 QY 2074 ATGCTGTTATGAGTGGCTT-TAATGAATAAATTT 2108
 Db ATGCTGTTATGAGTGGCTT-TAATGAATAAATTT 1
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 Bx415858/c
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 DEFINITION 3-PRIME, mRNA sequence.
 ACCESSION Bx415858
 VERSION Bx415858.2 GI:46955857
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 918)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 15, 2003 this sequence version replaced gi:30767592.
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 This sequence belongs to sequence cluster 1670.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0CAP008B10NP1&c=1670.r.

FEATURES
 Location/Qualifiers
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/clone="CS0CAP008YC20"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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| Query Match | 36.9%; Score 834.4; DB 4; Length 918; |
| Best Local Similarity | 91.6%; Pred. No. 2.2e-148; |
| Matches 841; Conservative 30; Mismatches 47; Indels 0; Gaps 0; | |
| Qy | 1184 AAAGCCAGACAGCTTTGATCAAAGGCACACAGCAGCTGAGTGTGGAGCAGTAGCTGG 1243 |
| Db | 918 AAATCCCAKARACAKNTGAAACAAAGKAMACAGCAAGAMAKGGTTTWTWTRTTMTTK 859 |
| Qy | 1244 AGGACCTTGTCTCCAGCTCAGGCTCTTTCTCCACACACCTTCAGTCTTTCTTTCCG 1303 |
| Db | 858 WTTKACCAATTCYCCCGCTCATKCTCNMCMACACCAACATGCGNCNCNAMWCK 799 |
| Qy | 1304 AGGCCCTGTCTCAGGGTGTCTGAGTCTCAACGGCAAGGGAACAAGTACTTCTT 1363 |
| Db | 798 ATGCCCTGACACWTTKTTWTKTGTCTGTTGCCCACTKATTTKAAAGTACTTCTT 739 |
| Qy | 1364 GATACCTGGGATCTGTGCCAGACCTCGAGGAGGTAATGAATTAAGAAAGAACTGC 1423 |
| Db | 738 GATACCTGGGATCTGTGCCAGACCTCGAGGAGGTAATGAATTAAGAAAGAACTGC 679 |
| Qy | 1424 CTTTGGCAGAGTCTATATGTAACATATCAGACTTTTTTTTTTTTATATCAAGCTA 1483 |
| Db | 678 CTTTGGCAGAGTCTATATGTAACATATCAGACTTTTTTTTTTTTATATCAAGCTA 619 |
| Qy | 1484 AAATGTATGACCTTAAATAAATGAAGTGTGAGCTTAACCTCGAAATGAATCCCT 1543 |
| Db | 618 AAATGTATGACCTTAAATAAATGAAGTGTGAGCTTAACCTCGAAATGAATCCCT 559 |
| Qy | 1544 CTATCTCTAAAGAAAATCTCTGTGAAACCCCTATGTGGAGGCGGAATGTCTCCAGCC 1603 |
| Db | 558 CTATCTCTAAAGAAAATCTCTGTGAAACCCCTATGTGGAGGCGGAATGTCTCCAGCC 499 |
| Qy | 1604 CTTGATTCAGAGGGGCCATGAAGAGGACAGCTACCCCTTTACAAATAGATTTGA 1663 |
| Db | 498 CTTGATTCAGAGGGGCCATGAAGAGGACAGCTACCCCTTTACAAATAGATTTGA 439 |
| Qy | 1664 GCATCAGTGAGGTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTT 1723 |
| Db | 438 GCATCAGTGAGGTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTT 379 |
| Qy | 1724 CTTGGATCACTGATGACTTTTATATCTTTGTAAGACAATTTGTTGGAGACCCCTACA 1783 |
| Db | 378 CTTGGATCACTGATGACTTTTATATCTTTGTAAGACAATTTGTTGGAGACCCCTACA 319 |
| Qy | 1784 CAGCCCTGGCTCTGCTCAACTAGCAGATACAGGATGAGCAGACCTGACTCTTTAAG 1843 |
| Db | 318 CAGCCCTGGCTCTGCTCAACTAGCAGATACAGGATGAGCAGACCTGACTCTTTAAG 259 |
| Qy | 1844 GAGGCTGAGAGCCCAAACTGTCTGCCAAAATGCACTTCTCTGTTAAGGTATGGTACA 1903 |
| Db | 258 GAGGCTGAGAGCCCAAACTGTCTGCCAAAATGCACTTCTCTGTTAAGGTATGGTACA 199 |
| Qy | 1904 AGCAATGCTGCCCATTCGGAGAGAAAACTTAACTAGTAGATAGGAAATAAGAACCACTCA 1963 |
| Db | 198 AGCAATGCTGCCCATTCGGAGAGAAAACTTAACTAGTAGATAGGAAATAAGAACCACTCA 139 |
| Qy | 1964 TAAATCTTCACTTAGGTAATCTCTGTTTAAATATGTTGATACATCTTCTGATTTATTT 2023 |
| Db | 138 TAAATCTTCACTTAGGTAATCTCTGTTTAAATATGTTGATACATCTTCTGATTTATTT 79 |
| Qy | 2024 TCTACACATACATGTAATAATATGCTTTCTTTTTTAAATAGGGTTGTACTATGCTGTTAT 2083 |
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| Qy | 2084 GAGTGGCTTTAATGAATA 2101 |
| Db | 18 GAGTGGCTTTAATGAATA 1 |
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| BI820267 | |
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| DEFINITION | mRNA sequence. |
| ACCESSION | BI820267 |
| VERSION | BI820267.1 GI:15931817 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; |
| | Hominidae; Homo. |
| REFERENCE | 1 (bases 1 to 882) |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/. |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) |
| JOURNAL | Unpublished (1999) |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: csapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Plate: LLAM11443 row: g column: 06 High quality sequence stop: 769. |
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| | /lab_host="DH10B" |
| | /clone_lib="NIH_MGC_115" |
| | /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library." |
| ORIGIN | |
| Query Match | 34.8%; Score 786.6; DB 2; Length 882; |
| Best Local Similarity | 97.0%; Pred. No. 2.8e-139; |
| Matches 855; Conservative 0; Mismatches 13; Indels 7; Gaps 5; | |
| Qy | 63 CGCGCGCTCCCTCGCGCCCGAGCTTCGAGCAAGACGCGCTCTGGGAGCGCGTCATG 122 |
| Db | 1 CGCGCGCTCCCTCGCGCCCGAGCTTCGAGCAAGACGCGCTCTGGGAGCGCGTCATG 60 |
| Qy | 123 GCCT-TACCACTGACCGCTTGTCTTCCCGCTGGCTTGTGTCTTCCACGCCCGCAGGCC 181 |
| Db | 61 GCCTATACCACTGACCGCTTGTCTTCCCGCTGGCTTGTGTCTTCCACGCCCGCAGGCC 120 |
| Qy | 182 GAGCAGTTCGGGTGTCCGCGCTGGATCGGACCTCGGAACCTGGCGGAGACAGTGGAGCT 241 |
| Db | 121 GAGCAGTTCGGGTGTCCGCGCTGGATCGGACCTCGGAACCTGGCGGAGACAGTGGAGCT 180 |
| Qy | 242 GAAATGCCAGGTGTGTGTGTCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCCGG 301 |
| Db | 191 GAAATGCCAGGTGTGTGTGTCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCCGG 240 |

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| High quality sequence stop: 788. | |
| Location/Qualifiers | |
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| /lab_host="DH10B" | |
| /clone_lib="NIH_MGC_115" | |
| /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library." | |
| ORIGIN | |
| Query Match 34.3%; Score 775.4; DB 2; Length 789; | |
| Best Local Similarity 99.7%; Pred No 3.8e-137; | |
| Matches 787; Conservative 0; Mismatches 1; Indels -1; Gaps 1; | |
| QY | 45 CGGCGCCACCGGCTCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGT 104 |
| Db | 1 CGGCGCCACCGGCTCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGT 60 |
| QY | 105 CTGGGGAGCGGCTCATGGCTTACAGTGACCGCTTGCTCTGCGCGCTGGCTTGGCTG 164 |
| Db | 61 CTGGGGAGCGGCTCATGGCTTACAGTGACCGCTTGCTCTGCGCGCTGGCTTGGCTG 120 |
| QY | 165 CTCACGCGCGCCAGCGCGGCTTCGCGGTGTCGCGCTGATCGGACCTGGAACTCG 224 |
| Db | 121 CTCACGCGCGCCAGCGCGGCTTCGCGGTGTCGCGCTGATCGGACCTGGAACTCG 180 |
| QY | 225 GCGGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGCTCCAAACCCGACGCTCGGCTGCTCG 284 |
| Db | 181 GCGGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGCTCCAAACCCGACGCTCGGCTGCTCG 240 |
| QY | 285 TGGCTCTTCAGCGCGCGCGCGCGCGCTTCCTCTCTATACCTCTCTCCCAA 344 |
| Db | 241 TGGCTCTTCAGCGCGCGCGCGCGCGCTTCCTCTCTATACCTCTCTCCCAA 300 |
| QY | 345 AACAGCCCAAGCGCGCGCGCGCTGGACACCCAGCGGCTTCGCGGCAAGAGTTGGG 404 |
| Db | 301 AACAGCCCAAGCGCGCGCGCGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGG 360 |
| QY | 405 GACACCTTCGCTCTCACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGC 464 |
| Db | 361 GACACCTTCGCTCTCACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGC 420 |
| QY | 465 TCGCGCTGAGCACTCCATCATGTATCTAGCCACTTCGTCGCGCGCTTCCTCGCAGCG 524 |
| Db | 421 TCGCGCTGAGCACTCCATCATGTATCTAGCCACTTCGTCGCGCGCTTCCTCGCAGCG 480 |
| QY | 525 AAGCCACACGAGCG 584 |
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| QY | 585 CCCCTGCTCCG 643 |
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| QY | 644 GGGGCTGAGCTTCGCTGTGATATCATCTGGCGCGCTTCGGCGCGGACTTGTGGGT 703 |
| Db | 601 GGGGCTGAGCTTCGCTGTGATATCATCTGGCGCGCTTCGGCGCGGACTTGTGGGT 660 |
| QY | 704 CTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763 |
| Db | 661 CTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720 |
| QY | 302 CGGCGCGCGCGCGAGTCCACCTTCCTCTATACCTCTCCCAAAACGAGCCAAAGCGCG 361 |
| Db | 241 CGGCGCGCGCGCGAGTCCACCTTCCTCTATACCTCTCCCAAAACGAGCCAAAGCGCG 300 |
| QY | 362 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCGCTCTAC 421 |
| Db | 301 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCGCTCTAC 360 |
| QY | 422 CTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGCGGCTGAGCAATC 481 |
| Db | 361 CTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGCGGCTGAGCAATC 420 |
| QY | 482 CATCATGTACTTACGACCTTCGTCGGTCTTCCTCGAGCGAAGCCACCAACGAGCG 541 |
| Db | 421 CATCATGTACTTACGACCTTCGTCGGTCTTCCTCGAGCGAAGCCACCAACGAGCG 480 |
| QY | 542 AGCGCGCGCACCAACACCGCGCGCCACCATCGGTCGAGCGCCCTGTCCTCGCGCC 601 |
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| QY | 602 AGAGGCGTTCG 661 |
| Db | 541 AGAGGCGTTCG 600 |
| QY | 662 TGATATCTACATCTGGCGCGCTTCGCGCGGACTTGTGGGTCTCTCTCTGTCAC 720 |
| Db | 601 TGATATCTACATCTGGCGCGCTTCGCGCGGACTTGTGGGTCTCTCTCTGTCAC 660 |
| QY | 721 TTATCACCTTTACTGCAACACAGGAGCGAGTGTTCGAAATGTCGCGCGCTG 780 |
| Db | 661 TTATCACCTTTACTGCAACACAGGAGCGAGTGTTCGAAATGTCGCGCGCTG 720 |
| QY | 781 TGGTCAAAATCGGG--AGACAAGCCAGCGCTTCGCGGAGATAGCTCAACCC--TGTGCA 836 |
| Db | 721 TGGTCAATCGGGGAGACAATGCGCCAGCTTCGCGGAGATAGCTCAACCCGTGTGCA 780 |
| QY | 837 ACAGCCACTAC--ATTACTTCAAACTGAGATCTCTCTTTGAGGAGCAAGTCTTCTCT 895 |
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| QY | 896 TTCAATTTTTCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 936 |
| Db | 841 TTCAATATTACAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 881 |
| RESULT 5 | |
| BI819839 | |
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| DEFINITION | |
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| ACCESSION | |
| BI819839 | |
| VERSION | |
| BI819839.1 GI:15931389 | |
| KEYWORDS | |
| SOURCE | |
| ORGANISM | |
| Homo sapiens (human) | |
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| Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | |
| Hominidae; Homo. | |
| 1 (bases 1 to 789) | |
| NIH-MGC http://mgc.nci.nih.gov/. | |
| National Institutes of Health, Mammalian Gene Collection (MGC) | |
| Unpublished (1999) | |
| Contact: Robert Strausberg, Ph.D. | |
| Email: c9apbs-r@mail.nih.gov | |
| Tissue Procurement: Life Technologies, Inc. | |
| cDNA Library Preparation: Life Technologies, Inc. | |
| cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) | |
| DNA Sequencing by: Incyte Genomics, Inc. | |
| Clone distribution: MGC clone distribution information can be | |
| found through the I.M.A.G.E. Consortium/LLNL at: | |
| http://image.llnl.gov | |
| Plate: LLAM11454 row: d column: 18 | |

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Qy 764 CAATGTCCCGGCTGTGGTCAATCGGGAGACAAGCCAGCCTTTTCGGCGAGATACGT 823
Db 721 CAATGTCCCGGCTGTGGTCAATCGGGAGACAAGCCAGCCTTTTCGGCGAGATACGT 780

Qy 824 CTAACCCCTG 832
Db 781 CTAACCCCTG 789

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LOCUS DA931234 SPLEN1 Homo sapiens cDNA clone SPLN1000141 5', mRNA
DEFINITION DA931234 sequence.
ACCESSION DA931234
VERSION DA931234.1 GI:82056788
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 838)
Kimura K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakeguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@ifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
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ORIGIN
Query Match          33.8%; Score 764.8; DB 9; Length 838;
Best Local Similarity 99.4%; Pred. No. 4e-135;
Matches 777; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 32 AACTTTCCCTCGGCGCCACCGGTCCGCGCGCTCCCTCGGCGCGAGCTTCG 91
Db 1 AACTTTCCCTCGGCGCCACCGGTCCGCGCGCTCCCTCGGCGCGAGCTTCG 60

Qy 92 ACCAAGACGCTCTGGGGAGCGGTCTATGCGCTTACAGTACGCGCTTCTCTGCC 151
Db 61 AGCCAAGACGCTCTGGGGAGCGGTCTATGCGCTTACAGTACGCGCTTCTCTGCC 120

Qy 152 GCTGGCCTTGCTGCTCCAGCGCCGAGCGGAGCAGTCCCGGTGTCGCGCTGGATCG 211
Db 121 GCTGGCCTTGCTGCTCCAGCGCCGAGCGGAGCAGTTCGCGGTGTCGCGCTGGATCG 180

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Qy 212 GACCTGAACTCGGCGAGACAGTGGAGCTGAAGTGCACAGTGTCTGTCGAACCCGAC 271
Db 181 GACCTGAACTCGGCGAGACAGTGGAGCTGAAGTGCACAGTGTCTGTCGAACCCGAC 240

Qy 272 GTGGGCTGCTCGTGGCTCTTTCAGCGCGCGCGCGCGCCAGTCCACCTTCTCTCT 331
Db 241 GTGGGCTGCTCGTGGCTCTTTCAGCGCGCGCGCGCGCCAGTCCACCTTCTCTCT 300

Qy 332 ATACCTCTCCCAAAACAGCCCAAGCGCGCGAGGGCTGGACACCCAGCGGTTCCTGGG 391
Db 301 ATACCTCTCCCAAAACAGCCCAAGCGCGCGAGGGCTGGACACCCAGCGGTTCCTGGG 360

Qy 392 CAAGAGGTGGGGAGACACCTTCCTCCTCAGCGACTTCGCGCCAGAGAAAGAGGG 451
Db 361 CAAGAGGTGGGGAGACACCTTCCTCCTCAGCGACTTCGCGCCAGAGAAAGAGGG 420

Qy 452 CTACTATTTCCTCGCGCCCTGAGCACTCCTCATGTACTTTCAGCCACTTTCGTGCCGGT 511
Db 421 CTACTATTTCCTCGCGCCCTGAGCACTCCTCATGTACTTTCAGCCACTTTCGTGCCGGT 480

Qy 512 CTTCCTGCGACGGAAGCCCAACACGAGCGCGCGAGCCACCAACACCGCGGCCAC 571
Db 481 CTTCCTGCGACGGAAGCCCAACACGAGCGCGCGAGCCACCAACACCGCGGCCAC 540

Qy 572 CATCGCTCGAGCGCCCTTCCTCGCGCCAGAGCGCTGCCGCGAGCGGGGGGGCGC 631
Db 541 CATCGCTCGAGCGCCCTTCCTCGCGCCAGAGCGCTGCCGCGAGCGGGGGGGCGC 600

Qy 632 AGTCACACGAGGGGGTGGACTTCGCTGTGATATCTACATCTGGGCGCCCTTCGCGCGG 691
Db 601 AGTCACACGAGGGGGTGGACTTCGCTGTGATATCTACATCTGGGCGCCCTTCGCGCGG 660

Qy 692 GACTTGTGGGTCTCTTCCTGTCTCAGTGGTATCACCTTTTACTGCAACACAGAAACCG 751
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Qy 752 AAGACGTTTGGAAATGTCGCCGCTGTGGTCAATCGGGAGACAGCCAGCTTTC 811
Db 721 AAGACGTTTGGAAATGT-CCCGGCTGTGGTCAATCGGGAGACAGCCAGCTTTC 779

Qy 812 GG 813
Db 780 GG 781

RESULT 7
BX437211/c
LOCUS BX437211 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YB16
DEFINITION 3-PRIME, mRNA sequence.
ACCESSION BX437211
VERSION BX437211.2 GI:47009751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30781554.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

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This sequence belongs to sequence cluster 1670.1
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSOCAP005DA08NP1&c=1670.1>.

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FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP005YB16"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 33.8%; Score 763.4; DB 4; Length 847;
Best Local Similarity 91.9%; Pred. No. 7.4e-135;
Matches 779; Conservative 47; Mismatches 19; Indels 3; Gaps 3;

QY 1263 TCAGGCTCTTCTCCACACCATTCAGGCTCTTCTTCGAGGCCCTGTCTCAGGGTG 1322
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
847 TCAGGCTTTTTCCTCCACACATTCAGGCTCTTCTTCGAGGCCCTGTCTCAGGGTG 788
QY 1323 AGGTGCTTGAGTCTCAACCGCAAGGAAACAAGTACTTCTGATACCTGGGATCTGTGC 1382
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
787 AGTGTGTTKATTYNCCACCGCAAGGNAAYAKTWTTTYTGATACYKGGATCTGKGC 728
QY 1383 CCAGAGCCTCGAGGAGTGAATGAAT-AAAGAAGAACTGCTTTGGCAGAGTCTATA 1441
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
727 CCAGAGCCTCGAGGAGTGAATGAATTAAGAAGAAACGCGCTTGGGCAGAGTCTATA 668
QY 1442 ATGTAACAATATCAGCTTTTCTTTTATATCAAGCTAAATTTGATAGACTTAA 1501
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
667 WTGTAAACATWTCARCTTTTCTTTTATATCAAGCTAAATTTGATAGACTTAA 608
QY 1502 ATAAATGAAGTGGTGAAGCTTAACCTCGAAATGAATCCCTCTATCTCTAAAGAAAATC 1561
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
607 WTAAATGAAGTGGTGAAGCTTAACCTCGAAATGAATCCCTCTWTYTCCTAAAGAAAT 548
QY 1562 TCTGTGAACCCCTATGTGGAGCGGAATGTCTCCAGCCCTGTCATTTGAGAGGGGC 1621
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
547 TTT-TGAACCCCTTGTGTGGAGCGGAATGTCTCCAGCCCTGTYTWTGAGAGGGGC 489
QY 1622 CCATGAAGAGCAGAGCTACCCCTTTACAATAGAAATTTGAGCATCACTGAGTTAAC 1681
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
488 CCATGAAGAGCAGAGCTACCCCTTTACAATAGAAATTTGAGCATCACTGAGTTAAC 429
QY 1682 TAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTCTGGGATCACTGATGAC 1741
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTCTGGGATCACTGATGAY 369
QY 1742 TTTTATATCTTTGTAAGAACAAATTTGAGAGCCCTCCACAGCCCTGGCCTCTGTCTC 1801
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 TTTTATATCTTTGTAAGAACAAATTTGAGAGCCCTCCACAGCCCTGGCCTCTGTCTC 309
QY 1802 TACTAGCATACAGGATGAGGACACCTGACTCTTTAAGAGGCTGAGAGCCCAAC 1861
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
308 AATAGCATACAGGATGAGGACACCTGACTCTTTAAGAGGCTGAGAGCCCAAC 249
QY 1862 TGCTGTCCCAACATGCACCTCTCTTGAAGTATGGTACAGCAATGCTCTGCCCATG 1921
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
248 TGTTGTCCCAACATGCACCTCTCTTGAAGTATGGTACAGCAATGCTCTGCCCATG 189
QY 1922 GAGAGAAAAAATTAAAGTATAGAAATAAGAACCACTATAATTTCTACCTTAGGA 1981
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 GAGAGAAAAAATTAAAGTATAGAAATAAGAACCACTATAATTTCTACCTTAGGA 129
QY 1982 ATAATCTCTGTTAATATGGTGTACATTTCTCTGATTAATTTTACACATCATGTAAA 2041
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 ATAATCTCTGTTAATATGGTGTACATTTCTCTGATTAATTTTCTACACATCATGTAAA 69
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QY 2042 ATATGTCTTTCTTTTAAATAGGTTGTACTATGCTGTTA-TGAGTGGCTTTAATGAAT 2100
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
68 ATATGTCTTTCTTTTAAATAGGTTGTACTATGCTGTTA-TGAGTGGCTTTAATGAAT 9

QY 2101 AAACATTT 2108
Db |::|||
8 AWAYTTT 1

RESULT 8
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LOCUS 603034019F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
DEFINITION mRNA sequence.
ACCESSION BI820808
VERSION BI820808.1 GI:15932358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11436 row: e column: 06
High quality sequence stop: 802.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5175149"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/notes="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 Kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 32.9%; Score 744.8; DB 2; Length 804;
Best Local Similarity 98.1%; Pred. No. 2.6e-131;
Matches 785; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

QY 123 GCCTTACCAGTGACCGCTTGCTCTGCGCTGGCTTGCTCTCCAGCCGCGAGCGCG 182
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 GCCTTACCAGTGACCGCTTGCTCTGCGCTGGCTTGCTCTCCAGCCGCGAGCGCG 63
QY 183 AGCCAGTTCCCGGTTGCTCGCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAGCTG 242
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 AGCCAGTTCCCGGTTGCTCGCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAGCTG 123
QY 243 AAGTCCAGGTTGCTGCTGTCCAAACCGAGCTGGGCTGCTGTGGCTCTTCCAGCGCGCG 302
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 AAGTCCAGGTTGCTGCTGTCCAAACCGAGCTGGGCTGCTGTGGCTCTTCCAGCGCGCG 183
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QY 303 GCGCGCGCGCGAGTCCACCTTCTCTATACCTTCCCAAAACAAGCCCAAGCGCGCC 362
Db 184 GCGCGCGCGCGAGTCCACCTTCTCTATACCTTCCCAAAACAAGCCCAAGCGCGCC 243
QY 363 GAGGGCTGGACACCCACGCGTTCGCGGCAAGAGTTGGGGACACCTTCTCTACCC 422
Db 244 GAGGGCTGGACACCCACGCGTTCGCGGCAAGAGTTGGGGACACCTTCTCTACCC 303
QY 423 CTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGCCCTGAGCAACTCC 482
Db 304 CTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGCCCTGAGCAACTCC 363
QY 483 ATCATGTACTTACGACACTTGTGCGCGTCTTCTGCGAGGAGCCCAACACGAGCGCA 542
Db 364 ATCATGTACTTACGACACTTGTGCGCGTCTTCTGCGAGGAGCCCAACACGAGCGCA 423
QY 543 GCGCGCGACCAACAACCGCGCCCAACCATCGGTGCGAGCCCTGCTCCGCGCCA 602
Db 424 GCGCGCGACCAACAACCGCGCCCAACCATCGGTGCGAGCCCTGCTCCGCGCCA 483
QY 603 GAGCGTCCGCGCGCGCGCGCGCGAGTGACACAGAGGGGCTGGACTTCGCCCTGT 662
Db 484 GAGCGTCCGCGCGCGCGCGCGAGTGACACAGAGGGGCTGGACTTCGCCCTGT 543
QY 663 GATATCTACTTGGCGCGCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTACTGTT 722
Db 544 GATATCTACTTGGCGCGCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTACTGTT 603
QY 723 ATCACTTTACTGCAACACAGGAACGAGAGCGTTTGCAGATGTCGCCGCGCTGT 782
Db 604 ATCACTTTACTGCAACACAGGAACGAGAGCGTTTGCAGATGTCGCCGCGCTGT 663
QY 783 CTCAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCT-AAACCTGTGCAACAGC 841
Db 664 CTCAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAGC 723
QY 842 CACTACATTACTT-AACTGAGATCTTCTTTTGGAGGAGCAAGTCTTCCCTTTTCA 900
Db 724 CACTACATTACTTCAAACTGAGATCTTCTTTTGGAGGAGCAAGTCTTCCCTTTTCA 783
QY 901 TTTT-CCAGTCTTCTCC 919
Db 784 TTTTCCAGTCTTCTCC 803

RESULT 9
BI760947
LOCUS 603043151F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
DEFINITION mRNA sequence.
ACCESSION BI760947
VERSION BI760947.1 GI:15752525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: e column: 13
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High quality sequence start: 4
High quality sequence stop: 756.
Location/Qualifiers
1. 780

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183604"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 32.0%; Score 724.4; DB 2; Length 780;
Best Local Similarity 98.7%; Pred. No. 2e-127;
Matches 762; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

QY 54 ACCGGCTCCCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAAAGACGCTCTGGGAG 113
Db 1 ACCGGCTCCCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAAAGACGCTCTGGGAG 60

QY 114 CGGCTATGGCTTACAGTGACCGCTTGTCTCTCGCGCTGGCTTCTGCTTCCACGCC 173
Db 61 CGGCTATGGCTTACAGTGACCGCTTGTCTCTCGCGCTGGCTTCTGCTTCCACGCC 120

QY 174 GCCAGCGCGAGTTCGCGGTGTGCGCGCTGGATCGGACTCTGGAACCTGGGCGAGACA 233
Db 121 GCCAGCGCGAGTTCGCGGTGTGCGCGCTGGATCGGACTCTGGAACCTGGGCGAGACA 180

QY 234 GTGAGCTGAAGTCCAGGTCTCTGTGCCAACCGAGCTCGGGTGTCTGTGGTCTTTC 293
Db 181 GTGAGCTGAAGTCCAGGTCTCTGTGCCAACCGAGCTCGGGTGTCTGTGGTCTTTC 240

QY 294 CAGCGCGCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 353
Db 241 CAGCGCGCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300

QY 354 AAGCGCGCGAGGGCTGGACACCGCGGTTCCTCGGGCAAGAGGTGGGGGACACCTTTC 413
Db 301 AAGCGCGCGAGGGCTGGACACCGCGGTTCCTCGGGCAAGAGGTGGGGGACACCTTTC 360

QY 414 GTCTTCACTTCTGAGGCTTCCCGCGAGAGAACGAGGCTACTATTTCTGTCTGGCCCTG 473
Db 361 GTCTTCACTTCTGAGGCTTCCCGCGAGAGAACGAGGCTACTATTTCTGTCTGGCCCTG 420

QY 474 AGCAACTCATCATGTACTTTCAGCCACTTCTGCGCGTCTTCTTCTTCTTCTTCTTCTT 533
Db 421 AGCAACTCATCATGTACTTTCAGCCACTTCTGCGCGTCTTCTTCTTCTTCTTCTTCTT 480

QY 534 ACGAGCG 593
Db 481 ACGAGCG 540

QY 594 CTGCGCCCGAGAGGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 653
Db 541 CTGCGCCCGAGAGGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600

QY 654 TTGCGCTGTATCTTACTATCTGGCGCGCTTGGCGCGGAGCTTGTGGGTCTTCTTCTTCT 713
Db 601 TTGCGCTGTATCTTACTATCTGGCGCGCTTGGCGCGGAGCTTGTGGGTCTTCTTCTTCT 660

QY 714 TCACT--GGTTATCATCCCTTTTACTGCAACCAAGAGCGTGTTCGCAATGTC 771
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|-----------------------|--|--|----------------------------------|
| Db | 661 | TCACCTGGTTATACACCCCTTTACTGTCACACACAGAACCCGAGACGCTGTTTGC-AATGTC | 719 |
| Qy | 772 | CCCGGCTCTGGTCAAAATCGGAGACAAGCCAGCC-TTTCGGCGAGATACG | 822 |
| Db | 720 | CCCGGCTCTGGTCAAAATCGGAGACAAGCCAGCCCTTTTCGGCGAGATACG | 771 |
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| LOCUS | AW949684 | 749 bp mRNA linear | EST 01-JUN-2000 |
| DEFINITION | EST361754 | MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence. | |
| ACCESSION | AW949684 | | |
| VERSION | AW949684.1 | GI:8139317 | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | | | |
| AUTHORS | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | | |
| TITLE | Hegde, P., Qi, R., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J. | | |
| JOURNAL | Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray | | |
| COMMENT | Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 5 | | |
| Seq primer: | Reverse. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..749 | | |
| ORIGIN | | | |
| Query Match | 31.3%; | Score 708; | DB 7; Length 749; |
| Best Local Similarity | 98.5%; | Pred. No. 2.6e-124; | |
| Matches | 725; | Conservative 0; | Mismatches 10; Indels 1; Gaps 1; |
| Qy | 1000 | ACAAACTAGTAAATCTACAGTACACCAAGGTCACATCTGTTGGGCACATC | 1059 |
| Db | 1 | ACAAACTAGTAAATCTACAGTACACCAAGGTCACATCTGTTGGGCACATC | 60 |
| Qy | 1060 | GGGTAGGCGTGGAAAGGGCGAGCGTACCCGAGAGTCTCAGATCATGCTG | 1119 |
| Db | 61 | GGGTAGGCGTGGAAAGGGCGAGCGTACCCGAGAGTCTCAGATCATGCTG | 120 |
| Qy | 1120 | AGAGAGCTGGAGGCCACCATGTCATCTCAACCTCTTCCCGCCGCTTTACAAAGGGGA | 1179 |
| Db | 121 | AGAGAGCTGGAGGCCACCATGTCATCTCAACCTCTTCCCGCCGCTTTACAAAGGGGA | 180 |
| Qy | 1180 | GGCTAAAGCCAGAGACACTTGTATCAAGGACACAGCAAGTCAAGGTTGGAGCAGTAG | 1239 |
| Db | 181 | GGCTAAAGCCAGAGACACTTGTATCAAGGACACAGCAAGTCAAGGTTGGAGCAGTAG | 240 |
| Qy | 1240 | CTGGAGGACCTGTCTCCAGCTCAGGCTCTTCCCTCCACCATTCAGTCTTCTT | 1299 |
| Db | 241 | CTGGAGGACCTGTCTCCAGCTCAGGCTCTTCCCTCCACCATTCAGTCTTCTT | 300 |
| Qy | 1300 | TCGAGGCCCCCTGTCTCAGGCTGAGTGTCTGAGTCTCCACCGCAAGGGAACAAGTACT | 1359 |
| Db | 301 | TCGAGGCCCCCTGTCTCAGGCTGAGTGTCTGAGTCTCCACCGCAAGGGAACAAGTACT | 360 |
| Qy | 1360 | TCTTGATACCTGGGATCTGTGCCAGAGCTTCGAGGAGTGAATGAATTAAGAAGAGAA | 1419 |
| Db | | | |
| Db | 361 | TCTTGATACCTGGGATCTGTGCCAGAGCTTCGAGGAGTGAATGAATTAAGAAGAGAA | 420 |
| Qy | 1420 | CTGCGCTTTGGCAGAGTTCTATATATGTAACAATATCAGACTTTTTTTTTTAAATCAAG | 1479 |
| Db | 421 | CTGCGCTTTGGCAGAGTTCTATATATGTAACAATATCAGACTTTTTTTTTTAAATCAAG | 480 |
| Qy | 1480 | CCTAAATTTGTATAGACCTTAAATATAAATGAAGTGTGAGCTTAAACCTGGAAAAATGAAT | 1539 |
| Db | 481 | CCTAAATTTGTATAGACCTTAAATATAAATGAAGTGTGAGCTTAAACCTGGAAAAATGAAT | 540 |
| Qy | 1540 | CCCTCTATCTCTAAAGAAATCTCTGTGAACCCCTATGTGAGGCGGAATGCTCTCCC | 1599 |
| Db | 541 | CCCTCTATCTCTAAAGAAATCTCTGTGAACCCCTATGTGAGGCGGAATGCTCTCCC | 600 |
| Qy | 1600 | AGCCCTTGCATTCGAGAGGGGCCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAT | 1659 |
| Db | 601 | AGCCCTTGCATTCGAGAGGGGCCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAT | 660 |
| Qy | 1660 | TTGAGCATCAGTGAGGTTAAACTAAAGGCCCTTTGAATCTCTGAATTTGAG-ATACAAAC | 1718 |
| Db | 661 | TTGAGCATCAGTGAGGTTAAACTAAAGGCCCTTTGAATCTCTGAATTTGAGATACAAAC | 720 |
| Qy | 1719 | ATGTTCTCTGGATCAC | 1734 |
| Db | 721 | ATGTTCTCTGGATCAC | 736 |
| RESULT 11 | | | |
| LOCUS | BI911195 | 796 bp mRNA linear | EST 16-OCT-2001 |
| DEFINITION | 603062918F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211989 5', mRNA sequence. | | |
| ACCESSION | BI911195 | | |
| VERSION | BI911195.1 | GI:16174808 | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | | | |
| AUTHORS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | | |
| TITLE | NIH-MGC http://mgc.nci.nih.gov/. | | |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| COMMENT | Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs.r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1532 row: d column: 06 High quality sequence start: 29 High quality sequence stop: 791. Location/Qualifiers | | |
| FEATURES | 1..796 | | |
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| | /db_xref="taxon:9606" | | |
| | /clone="IMAGE:5211989" | | |
| | /tissue_type="leukocyte" | | |
| | /lab_host="DH10B" | | |
| | /clone_lib="NIH_MGC_118" | | |
| | /note="Vector: pCMV-SF076; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: | | |

| | | | | | | | | | |
|-----------------------------|---|---|-------------------|-------|-------------|----|--------|----|------|
| this is a NIH_MGC Library." | | | | | | | | | |
| ORIGIN | Query Match | 31.2% | Score 705.8; | DB 2; | Length 796; | | | | |
| | Best Local Similarity | 98.5%; | Pred. No. 7e-124; | | | | | | |
| | Matches | 765; | Conservative | 0; | Mismatches | 7; | Indels | 5; | Gaps |
| | | | | | | | | | |
| Qy | 1 | GAATTCAGGCTCCGGGCGCGCGGAGGCGCAACTTTTCCCTCCCTCGGGCCCCACCGGCT | 60 | | | | | | |
| Db | 20 | GGATTATGATCGGGCGCGCGGAGGCGCAACTTTTCCCTCCCTCGGGCCCCACCGGCT | 79 | | | | | | |
| | | | | | | | | | |
| Qy | 61 | CCCGGCGCCCTCCCTCGCGCC-CAGCTTCGAGCAGAGCGCTCTGGGGAGCGGCTC | 119 | | | | | | |
| Db | 80 | CCCGGCGCCCTCCCTCGCGCCCTGAGCTTCGAGCAGAGCGCTCTGGGGAGCGGCTC | 139 | | | | | | |
| | | | | | | | | | |
| Qy | 120 | ATGGCCTTACAGTAGACCGCTTGTCTCTCGCGCTGGCTTGGCTCTCCACGCGCCAGG | 179 | | | | | | |
| Db | 140 | ATGGCCTTACAGTAGACCGCTTGTCTCTCGCGCTGGCTTGGCTCTCCACGCGCCAGG | 199 | | | | | | |
| | | | | | | | | | |
| Qy | 180 | CCGAGCCAGTTCCGGGTTCGCGCTGGATCGGACCTGGAACTCTGGGCGAGACAGTGGAG | 239 | | | | | | |
| Db | 200 | CCGAGCCAGTTCCGGGTTCGCGCTGGATCGGACCTGGAACTCTGGGCGAGACAGTGGAG | 259 | | | | | | |
| | | | | | | | | | |
| Qy | 240 | CTGAAGTCCAGGTGCTCTCTCCAAACCGGACGTCGGCTCTCTGGCTCTTCCAGCG | 299 | | | | | | |
| Db | 260 | CTGAAGTCCAGGTGCTCTCTCCAAACCGGACGTCGGCTCTCTGGCTCTTCCAGCG | 319 | | | | | | |
| | | | | | | | | | |
| Qy | 300 | CGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAAACAAGCCCAAGCG | 359 | | | | | | |
| Db | 320 | CGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAAACAAGCCCAAGCG | 379 | | | | | | |
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| Qy | 360 | CCGAGGGGCTGGACACCCAGCGTTCTCGGGCAAGAGTTGGGGACACCTTCTGTCCTC | 419 | | | | | | |
| Db | 380 | CCGAGGGGCTGGACACCCAGCGTTCTCGGGCAAGAGTTGGGGACACCTTCTGTCCTC | 439 | | | | | | |
| | | | | | | | | | |
| Qy | 420 | ACCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCTCTGAGCAAC | 479 | | | | | | |
| Db | 440 | ACCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCTCTGAGCAAC | 499 | | | | | | |
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| Qy | 480 | TCCATCATGTACTTTCAGCACTTCTGCGGCTTCTCTGCCAGGAAAGCCCAACGACG | 539 | | | | | | |
| Db | 500 | TCCATCATGTACTTTCAGCACTTCTGCGGCTTCTCTGCCAGGAAAGCCCAACGACG | 559 | | | | | | |
| | | | | | | | | | |
| Qy | 540 | CCAGCGCGCGGACCAACACCGCG-CGCCACCATCGCGTGCAGCCCTGTCTCTCG | 598 | | | | | | |
| Db | 560 | CCAGCGCGCGGACCAACACCGCGTGCACCACTCGCGTGCAGCCCTGTCTCTCG | 619 | | | | | | |
| | | | | | | | | | |
| Qy | 599 | CCCAGAGCGTGCAGCGCGCGGCGGCGGAGTGCACAGAGGGGCTGGACTTCG- | 657 | | | | | | |
| Db | 620 | CCCAGAGCGTGCAGCGCGCGGCGGCGGAGTGCACAGAGGGGCTGGACTTCGC | 679 | | | | | | |
| | | | | | | | | | |
| Qy | 658 | CTGTGATATCTACATCTGGGCGCCCTTTGG-CGCGGACTTGTGGGGTCTTCTCTGTCA | 716 | | | | | | |
| Db | 680 | CTGTGATATCTACATCTGGGCGCCCTTGGCCCGGACTTGTGGGGTCTTCTCTGTCA | 739 | | | | | | |
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| Qy | 717 | CTGGTTATCACCTTTTATGCAACACAGGAACCGAAGCGTGTGCAATGTCCC | 773 | | | | | | |
| Db | 740 | CTGGTTATCACCTTTTATG-TAACACAGGAACCGAAGCGTGTGCAATGTCCC | 795 | | | | | | |
| | | | | | | | | | |
| RESULT 12 | CO646993 | | | | | | | | |
| LOCUS | ILLUMIGEN MCQ 39909 Katze MNPB2 Macaca mulatta cDNA clone | | | | | | | | |
| DEFINITION | IBIUM:22761.57 similar to Bases 4 to 915 highly similar to human CD8A (Hs.85258), mRNA sequence. | | | | | | | | |
| ACCESSION | CO646993 | | | | | | | | |
| VERSION | CO646993.1 | GI:50568487 | | | | | | | |
| KEYWORDS | Macaca mulatta (rhesus monkey) | | | | | | | | |
| SOURCE | Macaca mulatta | | | | | | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | | | | | | | |

| | |
|-----------|--|
| REFERENCE | Cercopithecidae; Cercopithecinae; Macaca. |
| AUTHORS | 1 (Bases 1 to 949) Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and Iadonato, S.P. Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Biol. 6 (7), R60 (2005) Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagness@illumigen.com Sequenced on 2004.05.27. 648 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org |
| TITLE | PCR Primers FORWARD: CCCTCACTAAGGGAACAAA BACKWARD: CACTATAGGCGAAATTGGGTA Insert Length: 949 Std Error: 0.00 Plate: CL000326 row: D column: 02 Seq primer: CCCTCACTAAGGGAACAAA POLYA=No. |
| JOURNAL | |
| PUBMED | |
| COMMENT | |
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| ORIGIN | Query Match 31.1%; Score 703.4; DB 8; Length 949; Best Local Similarity 98.4%; Pred. No. 2e-123; Matches 834; Conservative 0; Mismatches 96; Indels 13; Gaps 6; Qy 68 GCCTCCCTCGCGCGCGGAGCTTCGAGCCAGCAGCTCTCGGGAGCGGTCATGGCCTT 127 Db 4 GCCTCCCGTGGCGCGCGGAGCTTCTAGCCGAGCCGCGTCTGGGGAGCGGTCATGGCCCC 63 Qy 128 ACCAGTAGCCCTTGTCTCTCGCGCTGGCTTGTCTGCCACGCCGCGCCGAGCCA 187 Db 64 TCCGCTGNAACGCTTGTCTCTCGCGCTGTCTTGTCTGCCACGCCGCGCCAAACA 123 Qy 188 GTTCGGGTGTGCGCGTGGATCGGACCTGGAACCTGGGGGAGACAGTGGAGCTGAATG 247 Db 124 GTTCGAGTGTGCGCGCTGGGTTCGACCTGGAACCTGGGAGAGACGCTGAAGTG 183 Qy 248 CCAGTGTGCTGTCCACCCGAGCTGGGCTGTCTGGGCTCTTCCAGCGCGCGGCGC 307 Db 184 CCAGTGTGCTGTCCACCCGAGCTGGGCTGTCTGGGCTCTTCCAGCGCGCGGCGC 243 Qy 308 CGCGCCAGTCCCACTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGCGCGAGGG 367 Db 244 CGCGCGCGCGCGCGCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGCGCGAGGG 303 Qy 368 GCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGCTCCTACCTGAG 427 Db 304 GCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGCTCCTACCTACG 363 Qy 428 CGACTTCGCGCGAGAGAACGAGGGGCTACTATTTCTGCTCGGCGCTTGAGCAACTCCATCAT 487 |

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424 GTACTTCAGCCACTTCGTGCGGTCTTCTCGCAGCGAGGCCACACGACGCGCCGCGC 483
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724 AAATCGGAGAGCAAGCCCGCCCTTTCGGAAGATAGTCTTACCCCTGTGCAGAACCCAC 783
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784 TACTTTACTTCAAACTGAAACCTTTCTTTTGGGGAGCAAGCCCTTCCCTTTCCTTT 843
904 TTCCAGTCTTCCT-CCCTGTGTATTCATT-CTCATGATTAATTATTAGTGGG 954
844 TTTTCCAGTCTTCCCTTCCCTTATGATTCATTTCCTCCCTGGAATATTGTTTAAAGGG 903
955 GCGGGGTGGAAAGATTACTTTTCTTTATGTTGTTGAGGG 997
904 GCGGGGGGGGGGAAAAAATAATTTTCTTTTATGGG 946

RESULT 13

DN997301

LOCUS
DEFINITION

704 bp mRNA linear EST 17-MAY-2005
TC11602 Human breast cancer tissue, large insert, pcMV expression
library Homo sapiens cDNA clone TC11602 5' similar to Homo sapiens
CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 1,
mRNA sequence.

ACCESSION

DN997301.1 GI:66257128

EST.

Homo sapiens

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 704)
Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts

JOURNAL

COMMENT

Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606

Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.

FEATURES
source

Location/Qualifiers
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for large and GC rich mRNA transcripts, cDNA size
selection, optimized ligation for large inserts into
mammalian expression vector, random clones selected for
end sequence verification of full-length genes"

ORIGIN

Query Match 30.8%; Score 697; DB 9; Length 704;
Best Local Similarity 99.9%; Pred. No. 3.3e-122;
Matches 697; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 117 GTCATGGCTTACAGTGACCGCTTGTCTCGCTCGCTGGCTTGTCTCCACGCGCC 176
Db 67 GTCATGGCTTACAGTGACCGCTTGTCTCGCTCGCTGGCTTGTCTCCACGCGCC 126
QY 177 AGCCCGAGCAGTTCGCGGTGTGCGCGTGTGATCGGACCTGGAACCTGGCGGAGAGATG 236
Db 127 AGCCCGAGCAGTTCGCGGTGTGCGCGTGTGATCGGACCTGGAACCTGGCGGAGAGATG 186
QY 237 GAGCTGAAGTGCAGGTGCTGTCTCCAAACCGAGCTCGGGGTGCTGTGGTCTTCCAG 296
Db 187 GAGCTGAAGTGCAGGTGCTGTCTCCAAACCGAGCTCGGGGTGCTGTGGTCTTCCAG 246
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QY 357 CGCGCGCGCGCGCTGGACACCCAGCGGTTCGCGGCAAGAGGTGGGGGACACCTTCGTGTC 416
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QY 417 CTCACCTGAGCGACTTCGCGCGAGAGAAAGAGGCTACTATTTCTGCTCGGCCCTGAGC 476
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QY 477 AACTCATCATCTACTTCAGCCACTTCGTCGCGGTCTTCTCCAGCGAAGCCACACG 536
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QY 537 AGCCAGCG 596
Db 487 AGCCAGCG 546
QY 597 CGCCCGAGGCGTGCAGCG 656
Db 547 CGCCCGAGGCGTGCAGCG 606
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ORIGIN

Query Match 30.0%; Score 678.4; DB 1; Length 884;
Best Local Similarity 87.1%; Pred. No. 1.2e-118;
Matches 859; Conservative 2; Mismatches 8; Indels 117; Gaps 6;

QY 50 CCCACCGGCTCCCGCGCCCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCCCTGG 109
DB 1 CCCGACCGGCTCCCGCGCCCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCCCTGG 60

QY 110 GGAGCGGCTCATGGCTTACCAAGTACCGCCTTGCTTCGCGCTGGCCTTGCTGCTCCA 169
DB 61 GGAGCGGCTCATGGCTTACCAAGTACCGCCTTGCTTCCTGCGCTGGCCTTGCTGCTCCA 120

QY 170 CGCCGCCAGCGCCGAGCGAGTTCGGGTGTCGGCTGCGATCGGACCTGGAACTGGGGGA 229
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QY 230 GACAGTGGAGCTGAAGTGCAGGCTGCTGTCGTCGACCGAGCTGGGCTGCTGCTGCT 289
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QY 290 TTTCAGCGCGCGCGCGCGCGAGTCCCACTTCTCTCTATACCTCTCCCAAAACAA 349
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QY 410 TTTCGTCCTACCTGAGCGACTTCGCGGAGAGACGAGGCTACTATTTCTGCTCGGC 469
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QY 470 CTTGAGCAACTCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTCCAGCGAAGCC 529
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QY 530 CACCAAGCGCGCGCGCGCGACCAACACCGCGCGCCACCATCGGTCGCGAGCCCT 589
DB 478 CACCAAGCGCGCGCGCGCGACCAACACCGCGCGCCACCATCGGTCGCGAGCCCT 537

QY 590 GTCCCTGCGCGAGAGGCTGCGCGCGCGCGCGCGCGCGCGCGAGTGCACAGAGGGGCT 649
DB 538 GTCCCTGCGCGAGAGGCTGCGCGCGCGCGCGCGCGCGCGCGAG----- 581

QY 650 GGACTTCGCTGTGATATCATCTGCGCGCGCTTGGCGCGGACTTGTGGGTCCTTCT 709
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QY 770 TCCCGCGCTGTGGTCAATCGGGAGACAGCCGAGCTTTCGGCGAGATAGTCTTAACC 829
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QY 830 CTGTGCAACAGCGACTACATTACTTCAAACTGAGATCTTCC- TTTTGGAGGAGCAAGTC 888
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QY 889 CTTCCCTTTCAATTTTTCCAGCTTTCTCCCTGCTGATTCATCTCATGATTATTTT 948

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DB 787 AGTGGGGCGGGTGGGAAAGATTACTTTTCTTTATGTGTTTGACGGGAAACAAA-CT 844
QY 1009 GGTAAATCTACAGTACACCAAGG 1034
DB 845 AGTAAATCTACAGTACACCAAGG 870

Search completed: May 30, 2006, 09:48:04
Job time : 9655 secs

OLDEN KIDNEY

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:10:08 ; Search time 5105.02 Seconds
(without alignments)
3720.338 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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14: gb om:*
15: gb ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1006.5 | 96.5 | 708 | 2 | CQ882036 Sequence |
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ALIGNMENTS

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LOCUS CQ882012
DEFINITION Sequence 4 from Patent WO2004083404.
ACCESSION CQ882012
VERSION CQ882012.1 GI:54034737
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

inches

REFERENCE 1
AUTHORS Qi,Y., Zhang,X. and Konigsberg,P.J.
TITLE Gene therapy vectors having reduced immunogenicity
JOURNAL Patent: WO 2004083404-A 4 30-SEP-2004;
Isogenis, Inc. (US)

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ORIGIN

Alignment Scores:

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Score: 1043.00 Matches: 198

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ORIGIN
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Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1
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Db 1 ATGGCTTACAGTACCGCTTCTCTCGCGTGGCTTGTCTCCACCGCCGCGAG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGGTGTGGTGGATCGACCTGGAACCTGGCGGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCAGGTGTGTGTCTCAACCGGACGTCGGGTGTCTGTGGCTTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGGCGCGCGCGAGTCCACCTTCTCTTATACCTCTCCAAACCAAGCCCAAGGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCGAGGGGCTGCACACCGAGCGTCTCGGCAAGAGGTTCGGGGACACCTTCTCTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGCCACATTCGTGCGGCTTCTCTGCCAGGAGCCCAACAGAG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGGGGCCACCATCGGCTGCAGCCCTGTCTCTCGCG 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGGGGTGCGCGCCAGCGCGGGGGCGGCGAGTGACACAGAGGGGGTGGACTTCGCC 540
QY 171 ----- 171
Db 541 TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACTG 600
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCTTTACTGCACACAGGAAACGAGACGTGTTGCAATATGTCCTCCCGGCT 660
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaAlaArgTyrVal 198

Db 661 GTGGTCARATCGGAGACAGCCAGCTTTCGGCGAGATACGTC 705
RESULT 4
BD226429
LOCUS
DEFINITION
Immunosuppression by blocking T cell co-stimulatory signal 2
(B7/CD28 interaction).
ACCESSION
BD226429
VERSION
BD226429.1 GI:33036199
KEYWORDS
JP 2002513568-A/8.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 773)
AUTHORS
Lechler,I.R. and Dorling,A.
TITLE
Immunosuppression by blocking T cell co-stimulatory signal 2
(B7/CD28 interaction)
JOURNAL
Patent: JP 2002513568-A 8 14-MAY-2002;
IMPERIAL COLLEGE INNOVATIONS LTD
COMMENT
OS Homo sapiens (human)
PN JP 2002513568-A/8
PD 14-MAY-2002
PF 30-APR-1999 JP 2000547221
PR 30-APR-1998 GB 9809280.2
PI IAN ROBERT LECHLER, ANTHONY DORLING
PC C12N15/09, A01K57/027, A61K31/7052, A61K35/14, A61K38/00 PC
, A61K39/395, A61K39/395,
PC A61K48/00, A61P37/06, A61P43/00, C07K14/705, C07K16/28, C12N5/10,
PC C12N15/00,
PC A61K37/02, C12N5/00
CC Immunosuppression by blocking T cell co-stimulatory signal 2
CC (B7/CD28
CC interaction)
FH Key Location/Qualifiers
FT source 1..773 /organism="Homo sapiens"
FEATURES
source
1..773
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1,38e-65 Length: 773
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1
US-10-804-763-3 (1-198) x BD226429 (1-773)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 37 ATGGCTTACAGTACCGCTTGTCTCTCGCGTGGCTTGTCTCCACCGCCGCGAG 96
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 97 CCGAGCCAGTTCGGGGTGTGGTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAG 156
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 157 CTGAAGTCCAGGTGTGTGTCTCAACCGGACGTCGGGTGTCTGTCTCTTCTCCAGCG 216
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 217 CGCGGCGCGCGCGAGTCCACCTTCTCTTATACCTCTCCCAACCAAGCCCAAGGCG 276
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

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Db      277  GCCAGGGGCTGGACACCCAGCGTTCTCGGCGAAGAGTTGGGGGACACCTTCTGTCCTC 336
Qy      101  ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db      337  ACCCTGAGGACTTCCGCGAGAGACAGAGGCTACTATTCTGCTCGGCCCTTGAGCAAC 396
Qy      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLeuProThrThr 140
Db      397  TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCTCGCAGGAGGCCACCAACGACG 456
Qy      141  ProIleProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      457  CCAGCGCGGACCAACCAACCGCGCCCAACCATCGCGTCCGAGCCCTGTCCCTGCGC 516
Qy      161  ProGluAlaCysArgProAlaAlaGlyAla----- 171
Db      517  CCAGAGGCGTCCGCGCAGCGCGGGGGGCGCAGTGCAACAGAGGGGCTGGACTTCGCC 576
Qy      171  ----- 171
Db      577  TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACTG 636
Qy      172  -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db      637  GTTATCACCTTTACTGCAACACAGGAACGAAGACGTGTTGCAAAATGTCCTCGGCCCT 696
Qy      184  ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      697  GTGGTCAATCGGAGACAGCCAGCCCTTTTCGGCGAGATACGTC 741
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RESULT 5
AX011079          AX011079          773 bp      DNA      linear      PAT 06-SEP-2000
LOCUS
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DEFINITION      Sequence 16 from Patent WO957266.
ACCESSION      AX011079
VERSION        AX011079.1  GI:9997709
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KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
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```
REFERENCE
AUTHORS      Dorling, A. and Lechler, I. R.
TITLE        Immunosuppression by blocking t cell co-stimulation signal 2
              (b7/cd28 interaction)
JOURNAL      Patent: WO 957266-A 16 11-NOV-1999;
              IMP COLLEGE INNOVATIONS LTD (GB); DORLING ANTHONY (GB); LECHLER IAN
              ROBERT (GB)
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FEATURES
source        Location/Qualifiers
              1..773
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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ORIGIN
Alignment Scores:
Pred. No.:      1..386-65      Length:      773
Score:          1006.50      Matches:      197
Percent Similarity: 83.8%      Conservative: 0
Best Local Similarity: 83.8%      Mismatches: 1
Query Match:    96.5%      Indels:      37
DB:             2      Gaps:      1
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US-10-804-763-3 (1-198) x AX011079 (1-773)
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Qy      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      37  ATGGCTTACAGTACCGCTTGTCTCGCGCTTGTCTGCTCGCGCTTGTCTGCTCGCGCCAGG 96
Qy      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyCluThrValGlu 40
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```
Db      97  CCGAGCCAGTTCGGGGTGTCCGCCCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 156
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Qy      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      157  CTGAAGTCCAGAGTGCTGTGTCCAAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 216
```

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Qy      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      217  CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 276
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Qy      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      277  GCCAGGGGCTGGACACCCAGCGTTCTCGGCGAAGAGTTGGGGGACACCTTCTGCTCTC 336
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Qy      101  ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      337  ACCCTGAGCGACTTCCGCGAGAGAAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 396
```

```
Qy      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLeuProThrThrThr 140
Db      397  TCCATCATGTACTTCAGCCACTTCTGCGCGGCTTCTTCGCGAGGAAGCCCAACGACG 456
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Qy      141  ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      457  CCAGCGCGGACCAACCAACCGCGGCCCAACCATCGCGTCCGAGCCCTGTCCCTGCGC 516
```

```
Qy      161  ProGluAlaCysArgProAlaAlaGlyAla----- 171
Db      517  CCAGAGGCGTCCGCGCAGCGCGGGGGCGCAGTGCAACAGAGGGGCTGGACTTCGCC 576
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Qy      171  ----- 171
Db      577  TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 636
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Qy      172  -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db      637  GTTATCACCTTTACTGCAACACAGGACCGAGCGCTTTTGCNAATGTCCTCGGCCCT 696
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Qy      184  ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      697  GTGGTCAATCGGAGACAGCCAGCCCTTTTCGGCGAGATACGTC 741
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RESULT 6
CQ725925          CQ725925          1059 bp      DNA      linear      PAT 03-FEB-2004
LOCUS
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DEFINITION      Sequence 11859 from Patent WO02068579.
ACCESSION      CQ725925
VERSION        CQ725925.1  GI:42287423
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KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
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REFERENCE
AUTHORS      Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE        Kits, such as nucleic acid arrays, comprising a majority of
              humanexons or transcripts, for detecting expression and other uses
              thereof
JOURNAL      Patent: WO 02068579-A 11859 06-SEP-2002;
              PE Corporation (NY) (US)
              Location/Qualifiers
              1..1059
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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ORIGIN
Alignment Scores:
Pred. No.:      1.81e-65      Length:      1059
Score:          1006.50      Matches:      197
Percent Similarity: 83.8%      Conservative: 0
Best Local Similarity: 83.8%      Mismatches: 1
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Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x CQ725925 (1-1059)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 65 ATGGCCCTTACAGTACCGCTTGTCTCGCGCTGTCTGTCTCCACGCGCGCAGG 124

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTriAsnLeuGlyGluThrValGlu 40
DB 125 CCGAGCGAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 184

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 185 CTGAAGTGCAGGTGCTGCTGCCAACCCGACGTCGGGCTGTCTGTGGCTCTTCCAGCGG 244

QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrlSerGlnAsnLysProLysAla 80
DB 245 CGCGGGCGCGCCAGTCCACCTTCTCTATAGCTCTCCCAAAACAAGCCCAAGGCG 304

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 305 GCGAGGGGCTGGACACCGCGGTCTCGGCAAGAGGTGGGGACACCTTCGTCTCTC 364

QY 101 ThrLeuSerAspPheArgArgGluAenGluGlyTyrlTyrlPheCysSerAlaLeuSerAsn 120
DB 365 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGTCTCGGCCCTGAGCAAC 424

QY 121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 425 TCATCATGTACTTACGACACTTCGTGCGGCTTCTCTGCGAGGAAGCCACACGAGCG 484

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 485 CAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCCCTGCGC 544

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 545 CCAGAGCGGTGCGCGCCAGCGGGCGGCGCAGTGCACACGAGGGGGCTGGACTTCGCC 604

QY 171 ----- 171

DB 605 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCTGCTG 664

QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
DB 665 GTTATCACCTTTACTGCAACCAACAGAACCCGAGACGTGTTTGCAAAATGTCCCCGCGCT 724

QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrlVal 198
DB 725 GTGGTCAAAATCGGAGACAGCCACGCTTTCGGCGAGATACGTC 769

RESULT 7
LOCUS 123895
DEFINITION Sequence 11 from patent US 5540926.
ACCESSION 123895
VERSION 123895.1 GI:1603765
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Aruffo,A., Hollenbaugh,D. and Iedbetter,J.A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 11 30-JUL-1996;
FEATURES Location/Qualifiers
1..1060
/organism="unknown"
/mol_type="unassigned DNA"

source

ORIGIN

Alignment Scores:
Pred. No.: 1,81e-65 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x 123895 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 66 ATGGCCCTTACAGTACCGCTTGTCTCGCGCTGTCTGTCTCCACGCGCGCAGG 125

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTriAsnLeuGlyGluThrValGlu 40
DB 126 CCGAGCGAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 185

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTGCAGGTGCTGCTGCCAACCCGACGTCGGGCTGTCTGTGGCTCTTCCAGCGG 245

QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrlSerGlnAsnLysProLysAla 80
DB 246 CGCGGGCGCGCCAGTCCACCTTCTCTATAGCTCTCCCAAAACAAGCCCAAGGCG 305

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCGAGGGGCTGGACACCGCGGTCTCGGCAAGAGGTGGGGACACCTTCGTCTCTC 365

QY 101 ThrLeuSerAspPheArgArgGluAenGluGlyTyrlTyrlPheCysSerAlaLeuSerAsn 120
DB 366 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGTCTCGGCCCTGAGCAAC 425

QY 121 SerIleMetTyrlPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 426 TCATCATGTACTTACGACACTTCGTGCGGCTTCTCTGCGAGGAAGCCACACGAGCG 485

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCCCTGCGC 545

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 546 CCAGAGCGGTGCGCGCCAGCGGGCGGCGCAGTGCACACGAGGGGGCTGGACTTCGCC 605

QY 171 ----- 171

DB 605 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCTGCTG 665

QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
DB 666 GTTATCACCTTTACTGCAACCAACAGGAACCCGAGACGTGTTTGCAAAATGTCCCCGCGCT 725

RESULT 8
LOCUS AR380469
DEFINITION Sequence 1014 from patent US 6607879.
ACCESSION AR380469
VERSION AR380469.1 GI:40088103
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological
JOURNAL response gene expression
Patent: US 6607879-A 1014 19-AUG-2003;

Unclassified.

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Incyte Corporation; Palo Alto, CA
Location/Qualifiers
1..1060
/organism="unknown"
/mol_type="genomic DNA"

FEATURES
    source
        1..1060
            Length: 1060
            Score: 1006.50
            Percent Similarity: 83.8%
            Best Local Similarity: 83.8%
            Query Match: 96.5%
            Indels: 1
            Gaps: 1
            Mismatches: 0
            Matches: 197
            Conservative: 0

ORIGIN
Alignment Scores:
Pred. No.: 1
Score: 1006.50
Percent Similarity: 83.8%
Best Local Similarity: 83.8%
Query Match: 96.5%
Indels: 1
Gaps: 1

US-10-804-763-3 (1-198) x AR380469 (1-1060)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiaAlaAlaArg 20
Db 66 ATGGCTTTACAGTACCGCTTGTCTCGGCTGGCTTGTCTCCAGCCGCCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGACCTGGAACCTGGCGGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCCGAGGTCTCTGTCACACCGACGTCGGGTGCTCGTGGCTCTTCCAGCGG 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 246 CGCGGCGCGCGCGCGCTTCTCTCTATACCTCTCCAAAACAGCCCAAGCGG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGCGACTTCCGCGGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysPheProThrThr 140
Db 426 TCCATCATGTACTTCAGCCACTTCGTGGCGGTCTTCCTGCCAGCGACCCACACGAG 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACACCGCGCCACCATCGCGTCGACGCCCTGTCCCTCGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyAla----- 171
Db 546 CCAGAGGCGTCCGCGCCAGCGCGCGGGCGCAGTGCACACGAGGGGCTGGACTTCGCC 605
QY 171 ----- 171
Db 606 TGTGATATCTACATCTGGGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTGTCTACTG 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTTGCAAAATGCCCCGGCT 725
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 726 GTGGTCAATCGGGAGACAAGCCAGCCCTTTCGGCGGAGATACGTC 770

RESULT 9
LOCUS HUMATCT8A 1060 bp mRNA linear PRI 22-JUL-1996
DEFINITION Homo sapiens T-cell surface protein T8 mRNA.
ACCESSION M12828
VERSION M12828.1 GI:179145
KEYWORDS cell surface glycoprotein.
SOURCE Homo sapiens (human)
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JOURNAL Patent: WO 2004083404-A 2 30-SEP-2004;

Isogenis, Inc. (US)

FEATURES

source

Location/Qualifiers
1..2261
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 3,49e-65 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x CQ882010 (1-2261)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACCAGTACCGCCCTTCTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 179

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTCCCGCTGGATCGGACCTGGAACCTGGGGGACAGTGGAG 239

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTGCCAACCGAGCTGGGCTGCTGTGGCTCTTCCAGCG 299

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAACCAAGCCCAAGCG 359

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACCCAGCGGTCTCGGGCAAGAGTTGGGGGACACCTTCTGCTC 419

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 479

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCCAGCCACTTCTGCGCGTCTTCTGCGGCAAGCCCAACGACG 539

Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTGCAGCCCTGTCCCTGCGC 599

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 600 CCAGAGGCGTGGCGGCGCGCGGGGCGGAGTGACACAGAGGGGCTGGACTTCGCC 659

Qy 171 ----- 171

Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTCTTCTCTGCACTG 719

Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATACCCCTTACTGCNACACACAGGAACCGAAGACGTGTTGCAAAATGCCCCGGCT 779

Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 824

RESULT 12
AX764527
LOCUS AX764527 708 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 44 from Patent WO20102852.
ACCESSION AX764527
VERSION AX764527.1 GI:32258735

KEYWORDS

synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

1

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

Location/Qualifiers

1..708

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

1..708

/note="unnamed protein product; modified protein"

/codon_start=1

/transl_table=11

/protein_id="CAE00108.1"

/db_xref="GI:32258736"

/translation="MALPVTALLPLALLHAARPSQFRVSLDRTWNLGTVELKQ

VLLSNPTSGCSWLPQRAAASPTFLLYLNQNKPKAAEGLDTQFSGRLGDTFVLT

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PEACRPAGGAVHTRGLDFACDIYIWAFLAGTCGVLVLLSLVITLYCNHRRNRCKCP

RPVVKSGDKFSLSARYV"

ORIGIN

Alignment Scores:

Pred. No.: 2,13e-65 Length: 708

Score: 1003.50 Matches: 196

Percent Similarity: 83.8% Conservative: 1

Best Local Similarity: 83.4% Mismatches: 1

Query Match: 96.2% Indels: 37

DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x AX764527 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 1 ATGGCCTTACCAGTACCGCCCTTCTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 60

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DEFINITION Homo sapiens mutant CD8 alpha antigen (CD8A) mRNA, complete cds.
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VERSION AY039664.1 GI:14861039
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS de la Calle-Martin,O., Hernandez,M., Ordi,J., Casamitjana,N.,
Arostegui,J.I., Caragol,I., Ferrando,M., Labrador,M.,
Rodriguez-Sanchez,J.L. and Espanol,T.
Famillial CD8 deficiency due to a mutation in the CD8 alpha gene
J. Clin. Invest. 108 (1), 117-123 (2001)
11435463
TITLE Casamitjana,N., Arostegui,J.I. and de la Calle,O.
JOURNAL Direct Submission
REFERENCE Submitted (12-JUN-2001) Immunohematology, Centre de Transfusio i
JOURNAL Banc de Teixits, Pg. de la Vall d'Hebron 119-129, Barcelona 08035,
Spain
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US-10-804-763-3 (1-198) x AY039664 (1-1018)

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DEFINITION Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript
variant 1, mRNA (cDNA clone MGC:34614 IMAGE:5227906), complete cds.
ACCESSION BC025715
VERSION BC025715.1 GI:193444021
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2150)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

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Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 2150)
Strausberg,R.
Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Akteer,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Green,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laxic,P., Legaspi,R., Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
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Alignment Scores:
Pred. No.: 1.55e-64 Length: 2150
Score: 997.50 Matches: 196
Percent Similarity: 83.4% Conservative: 0
Best Local Similarity: 83.4% Mismatches: 2
Query Match: 95.6% Indels: 37
DB: 5 Gaps: 1

US-10-804-763-3 (1-198) x BC025715 (1-2150)

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VERSION CQ843147.1 GI:50894934
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REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.

Full-length human cDNA

Patent: EP 1440981-A 1794 28-JUL-2004;

Research Association for Biotechnology (JP)

FEATURES

Location/Qualifiers

Source

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US-10-804-763-3 (1-198) x Q0843147 (1-3048)

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Title: US-10-804-763-3

Perfect score: 1043

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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| 32 | 816.5 | 78.3 | 3407 | 14 | AED96285 | Aed96285 Human C-r |
| 33 | 816.5 | 78.3 | 3743 | 14 | AED96281 | Aed96281 Human C-r |
| 34 | 804 | 77.1 | 597 | 13 | ADS92795 | Ad92795 Nucleotid |
| 35 | 804 | 77.1 | 597 | 13 | ADS19441 | Ad92795 DNA of th |
| 36 | 782 | 75.0 | 3476 | 14 | AED96284 | Aed96284 Human C-r |
| 37 | 637 | 61.1 | 366 | 2 | AAx80968 | Aax80968 Expressed |
| 38 | 634 | 60.8 | 363 | 8 | ABz69261 | Abz69261 Human CD8 |
| 39 | 620.5 | 59.5 | 785 | 13 | ADS92811 | Ad92811 Nucleotid |
| 40 | 620.5 | 59.5 | 785 | 13 | ADS19457 | Ad92811 DNA of th |
| 41 | 532 | 51.0 | 2001 | 13 | ADS92807 | Ad92807 Nucleotid |
| 42 | 532 | 51.0 | 2001 | 13 | ADS19453 | Ad92807 DNA of th |
| 43 | 510.5 | 48.9 | 1330 | 13 | ADS92805 | Ad92805 Nucleotid |
| 44 | 510.5 | 48.9 | 1330 | 13 | ADS19451 | Ad92805 DNA of th |
| 45 | 471.5 | 45.2 | 922 | 6 | ABL34273 | Ab134273 Human imm |

ALIGNMENTS

RESULT 1
ADS92793
ID ADS92793 standard; cDNA; 2150 BP.

XX

AC ADS92793;

XX 16-DEC-2004 (first entry)

DE cDNA of a secreted CD8 alpha-chain protein alternative transcript.

XX immune response; cell-specific antigen; allc antigen; CD8;

KW CD8 alpha chain; cellular immune response; humoral immune response;

XX transplacental allograft; graft-versus-host disease; transplacental; gene; ss.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 120...716

FT /*tag= a

FT /product= "CD8 alpha-chain"

XX WO2004083244-A2.

PD 30-SEP-2004.

XX 19-MAR-2004; 2004WO-US008574.

PF

XX

using related

Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 13
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-804-763-3 (1-198) x ADS19439 (1-2150)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACCACTGACCGCTTGTCTCCGCGTGGCTTGTCTCCAGCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGCGCGTGGATCGACCTTGGAACTTGGCGGAGAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGCTGCTCCACCGGACGTGGGTGCTGCTGGTCTTCCAGCGG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCGCTTCTCTCTATACCTTCTCCAAAACAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCGCGGTTCGCGGCAAGAGGTGGGGGACACCTTGGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTCTGCTCGGCTTGAACA 479
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTCTCCAGCGAAGCCCAAGCGAG 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGCGGTGCG 659
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 198
Db 660 CCCCCTGTGTGTGTCATTCGGGAGACAGCCAGCGCTTTCGGCGAGATAGTC 713

RESULT 3

ADZ26403
ID ADZ26403 standard; cDNA; 2150 BP.

XX AC ADZ26403;

XX DT 16-JUN-2005 (first entry)

XX DE Human CD8 cDNA.

XX KW cell culture; stem cell; CD8; ss; gene.

XX OS Homo sapiens.

XX PN WO2005030999-A1.

XX PD 07-APR-2005.

XX PF 24-SEP-2004; 2004WO-US031524.

XX PR 25-SEP-2003; 2003US-0506221P.

XX PR 08-OCT-2003; 2003US-0509594P.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PI Ritz J, Wu CJ;

XX WPI; 2005-273394/28.
DR P-PSDB; ADZ26404.

XX Detecting lineage-specific cells in a biological sample, useful for
PT determining the clinical outcome of a progenitor cell transfer in a
PT subject, comprises identifying lineage-specific mRNA in the sample.

PS Disclosure; SEQ ID NO 29; 393pp; English.

XX The invention relates to a method of detecting lineage-specific cells in
CC a biological sample which comprises identifying lineage-specific mRNA in
CC the sample. The methods are useful for determining the clinical outcome
CC of a progenitor cell transfer in a subject, and for identifying or
CC quantifying lineage-specific cells. The present sequence represents a
CC human cDNA that encodes a protein used to identify lineage-specific
CC cells.

SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-82e-67 Length: 2150
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-804-763-3 (1-198) x ADZ26403 (1-2150)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCTTACCACTGACCGCTTGTCTCCGCGTGGCTTGTCTCCAGCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGCGCGTGGATCGACCTTGGAACTTGGCGGAGAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGCTGCTCCACCGGACGTGGGTGCTGCTGGTCTTCCAGCGG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCGCTTCTCTCTATACCTTCTCCAAAACAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCGCGGTTCGCGGCAAGAGGTGGGGGACACCTTGGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTCTGCTCGGCTTGAACA 479
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTCTCCAGCGAAGCCCAAGCGAG 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGCGGTGCG 659
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 198
Db 660 CCCCCTGTGTGTGTCATTCGGGAGACAGCCAGCGCTTTCGGCGAGATAGTC 713

RESULT 4

AED96282
ID AED96282 standard; DNA; 3518 BP.

XX AC AED96282;
XX XX
XX DT 26-JAN-2006 (first entry)
XX XX
XX DE Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 439.
XX XX
XX XX Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
KW C-reactive protein pentraxin-related; CRP; genetic marker; ds.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO2005107364-A2.
XX XX
XX PD 17-NOV-2005.
XX XX
XX XX 27-JAN-2005; 2005WO-IB002407.
XX XX
XX PR 27-JAN-2004; 2004US-0539128P.
XX PR 27-JAN-2004; 2004US-0539129P.
XX PR 22-OCT-2004; 2004US-0620874P.
XX PR 22-OCT-2004; 2004US-0621004P.
XX PR 25-OCT-2004; 2004US-0621053P.
XX PR 25-OCT-2004; 2004US-0621072P.
XX PR 26-OCT-2004; 2004US-0621663P.
XX PR 27-OCT-2004; 2004US-0622016P.
XX PR 27-OCT-2004; 2004US-0622017P.
XX PR 27-OCT-2004; 2004US-0622320P.
XX PR 17-NOV-2004; 2004US-0628101P.
XX PR 17-NOV-2004; 2004US-0628112P.
XX PR 17-NOV-2004; 2004US-0628133P.
XX PR 17-NOV-2004; 2004US-0628134P.
XX PR 17-NOV-2004; 2004US-0628144P.
XX PR 17-NOV-2004; 2004US-0628145P.
XX PR 17-NOV-2004; 2004US-0628156P.
XX PR 17-NOV-2004; 2004US-0628165P.
XX PR 17-NOV-2004; 2004US-0628179P.
XX PR 17-NOV-2004; 2004US-0628190P.
XX PR 17-NOV-2004; 2004US-0628231P.
XX PR 17-NOV-2004; 2004US-0628251P.
XX PR 26-NOV-2004; 2004US-0630559P.
XX PR 08-DEC-2004; 2004US-0634075P.
XX PR 27-JAN-2005; 2005US-00043806.
XX XX
XX PA (COMP-) COMPUEN LTD.
XX PA (COHE/) COHEN Y.
XX XX
XX PI Toporik A, Pollock S, Levine Z, Avalon-Soffer M, Cojocaru GS;
XX PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX XX
XX DR WPI; 2005-810779/82.
XX XX
XX PT New polynucleotide, useful for diagnosing a CRP variant-detectable
XX PT disease or for selecting therapy for a CRP variant-detectable disease,
XX PT e.g., myocardial infarction, coronary artery disease.
XX XX
XX PS Disclosure; SEQ ID NO 439; 1670pp; English.
XX XX
XX CC The invention relates to a new isolated polynucleotide. The
XX CC polynucleotide is useful for diagnosing a CRP variant-detectable disease,
XX CC for monitoring disease progression or treatment efficacy or relapse of a
XX CC CRP variant-detectable disease or for selecting therapy for a CRP variant
XX CC -detectable disease, e.g., myocardial infarction, coronary artery
XX CC disease, non-fatal or fatal stroke, peripheral vascular disease,
XX CC congestive heart failure or sudden cardiac death. The present sequence
XX CC represents a human C-reactive protein, pentraxin-related (CRP) associated
XX CC marker DNA.

SQ Sequence 3518 BP; 766 A; 1056 C; 907 G; 789 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.18e-67 Length: 3518
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0
US-10-804-763-3 (1-198) x AED96282 (1-3518)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1608 ATGCCCTTACCAGTGACCGCCTTCTCTCGCGCTGGCTTCTCCAGCCCGCAGG 1667
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 1668 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGGGAACCTGGGCGACAGTGGAG 1727
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 1728 CTGAAGTGCCAGGTGCTGTCTCCAAACCCGACGTCGGGCTGCTCTCCAGCCG 1787
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 1788 CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAAAGCCCAAGCGC 1847
Qy 81 AlaGlyGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 1848 GCCGAGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTGGGGGACACCTTCCTCCTC 1907
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 1908 ACCCTGAGCGACTTCCGCCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 1967
Qy 121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 1968 TCCATCATGTACTTCAGCCACTTCTGTCGGTTCCTCGCCAGCGAAGCCCAACACGAGC 2027
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 2028 CCAGCGCGCGACCAACACCCGCGCCACCATCGGTGCGACGCCCTGTCCCTCGCGC 2087
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAlaGlyAsnArgArgValCysLysCys 180
Db 2088 CCAGAGCGGTCCGCGCCAGCGCGCGGGGGCGCAGGAAACCGAAGACGTGTTTGCAATGT 2147
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 198
Db 2148 CCCCAGCGCTGTGGTCAATCGGAGACAAAGCCAGCCCTTCGCGCGAGATACGTC 2201
RESULT 5
AAx80967
ID AAx80967 standard; cDNA; 708 BP.
XX
XX AC AAx80967;
XX
XX DT 18-AUG-1999 (first entry)
XX
XX DE Human CD8 alpha protein encoding cDNA.
XX
XX KW T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;
KW corticosteroid; human; CD8 alpha protein; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9921576-A1.
XX
XX PD 06-MAY-1999.
XX
XX PF 28-OCT-1998; 98WO-GB003235.

```
XX 28-OCT-1997; 97GB-00022779.
XX (ISIS-) ISIS INNOVATION LTD.
XX Jakobsen BK, Gao GF, Gerth UC, Sewell AK;
XX WPI; 1999-385058/32.
XX P-PSDB; AAY21688.
XX Inhibiting activity of T cells against target cells useful for treating
XX autoimmune diseases and allergy.
XX Disclosure; Fig 1A; 79pp; English.
XX The invention describes a method for inhibiting activity of T lymphocytes
XX against a target cell by treating the cell with a soluble form of a CD8
XX molecule. The method is used as immunosuppressive therapy, e.g. in
XX patients undergoing transplantation, but also for treating autoimmune
XX diseases and allergy, e.g. exacerbation of asthma caused by viral
XX infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
XX vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment
XX with CD8 protein provides more selective immunosuppression than use of
XX corticosteroids. The present sequence represents a cDNA encoding a human
XX CD8 alpha protein
XX
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-65 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x AAY80967 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACCAAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCACGCCGCGAG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTCGGCTGCGTGGATCGAGCTCGAACCTGGGCGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCAGGTGCTGTCTCCAAACCGGAGCTGCGGGTGTCTTCCAGCGC 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGGGCGCGCGCAGTCCGACCTTCTCTATACCTTCTCCAAAACAGGCCAAGGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCGAGGGGCGTGCACACCGCGGTCTCGGCAAGAGGTGGGACACCTTGTCTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCGAGAACGAGGGCTACTATTCTCGCGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTACGACACTTCGTGCGGCTCTCTGCGAGGAGGCCACACGAGCG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGCGTGCAGCCCTGTCTCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGGGCGTGCAGCGCGCGCGGGCGGCGAGTGCACACGAGGGGGGTGACTTCGCC 540
```

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QY 171 ----- 171
Db 541 TGTGATATACATCTGGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 600
QY 172 -----GlyAsnA:ArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCCCTTTACTTGCACACACAGAACCGAAGACGTGTTTGCAATGTCCCCGCGCT 660
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 661 GTGGTCAAAATCGGGAGACAAGCCCGCCCTTTCGGCGAGATACGTC 705
```

RESULT 6

ABZ69260

ID ABZ69260 standard; DNA; 708 BP.

XX AC ABZ69260;

XX DT 11-AUG-2003 (first entry)

XX DE Human CD8alpha chain coding sequence.

XX KW Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;

XX KW antiallergic; cytotoxic T cell response; inhibitor; gene; ds.

XX OS Homo sapiens.

XX PN WO2002102852-A2.

XX PD 27-DEC-2002.

XX PF 14-JUN-2002; 2002WO-GB002743.

XX PR 14-JUN-2001; 2001GB-00014533.

XX PA (AVID-) AVIDEX LTD.

XX PI Jakobsen BK, Glick M;

XX DR WPI; 2003-167488/16.

XX DR P-PSDB; AAO19807.

New modified CD8 molecule having enhanced binding to major histocompatibility complex, and having a Serine53 of at least one CD alpha chain is mutated to another amino acid, useful for treating e.g. graft rejection or hypersensitivity.

PS Disclosure; Fig 1A; 60pp; English.

The present invention provides modified human CD8 molecules whose binding to major histocompatibility complex (MHC) is enhanced compared to wild type CD8. The modified CD8 molecule or a corresponding nucleic acid is useful in medicine, particularly in manufacturing a medicament for modulating CD8+ T cell response. The modified CD8 proteins and nucleic acids encoding such proteins are useful in immunosuppressive therapy, particularly as inhibitors of cytotoxic T cell responses, and for treating autoimmune disorders, hypersensitivity (e.g. allergic reaction), graft versus host disease, or graft rejection. The present sequence is a CD8 coding sequence

SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2,55e-65 | Length: | 708 |
| Score: | 1006.50 | Matches: | 197 |
| Percent Similarity: | 83.8% | Conservative: | 0 |
| Best Local Similarity: | 83.8% | Mismatches: | 1 |
| Query Match: | 96.5% | Indels: | 37 |
| DB: | 8 | Gaps: | 1 |

US-10-804-763-3 (1-198) x ABZ69260 (1-708)

```
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCTTTACAGTGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGGGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGTTCTCGGCAAGAGTTGGGGACACCTTGTCTCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCTTGGCAAC 360
Qy 121 SerLeuMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCCATCATGTACTTTCAGCCACTTCTGTCGGCTTCTCCGCAAGAGTTGGGGACACCTTGTCTCTC 420
Qy 141 ProAlaProArgProProThrProAlaProThrTrpAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACCAACCGCGCGCCACCATCGCGTTCGACGCCCTGTCTCTGCGC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGGCGTGC CGCGCCAGCGCGCGGGCGCGCAGTGACACAGGGGGCTGGACTTGC 540
Qy 171 ----- 171
Db 541 TGTGATATCTACATCTGGCGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCTACTG 600
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCTTTACTGCAACACACAGGAAACCGAAGACGTGTTGGAAATGCTCCCGGCT 660
Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyTrpVal 198
Db 661 GTGGTCAAAATCGGGAGACAAAGCCAGCCTTTTCGGCGGAGATACGTC 705
RESULT 7
ADS92817
ID ADS92817 standard; cDNA; 708 BP.
XX
AC ADS92817;
XX
DT 16-DEC-2004 (first entry)
XX
DE Nucleotide sequence of a CD8 alpha-chain protein.
XX
KW immune response; cell-specific antigen; alloantigen; CD8;
KW CD8 alpha-chain; cellular immune response; humoral immune response;
KW transplant allograft; graft-versus-host disease; transplant; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..708
FT /tag= b
FT /product= "CD8 alpha-chain"
FT sig_peptide 1..63
FT /*tag= a
XX
PN WO2004083244-A2.
XX
```

```
PD 30-SEP-2004.
XX
XX 19-MAR-2004; 2004WO-US008574.
PF
XX
PR 19-MAR-2003; 2003US-0456378P.
XX
PA (ISOG-) ISOGENIS INC.
XX
XX Qi Y, Zhang X, Konigsberg PJ;
PI
XX WPI; 2004-691022/67.
DR
XX P-PSDB; ADS92816.
DR
XX Specifically inhibiting host immune responses to alloantigens, useful for
PT e.g. treating graft-versus-host disease, comprises contacting a target
PT cell expressing the antigen with an expression vector encoding a CD8
PT polypeptide.
XX
XX Disclosure; Fig 1; 98pp; English.
XX
XX The specification describes a method for specifically inhibiting a host
CC immune response to target cell-specific antigens (e.g. alloantigens). The
CC method comprises contacting a target cell expressing the antigen with an
CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
CC chain, where the CD8 polypeptide is expressed by the target cell and
CC where the host immune response against the target cell is specifically
CC inhibited. The method of the invention is useful for specifically
CC inhibiting both cellular and humoral immune responses to alloantigens,
CC thus finding use in extending the survival of transplant allografts and
CC in treating graft-versus-host disease in transplant recipients. The
CC present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
CC -chain may be used in the method of the invention.
XX
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,55e-65 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 13 Gaps: 1
US-10-804-763-3 (1-198) x ADS92817 (1-708)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCTTTACAGTGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGGGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGTTCTCGGCAAGAGTTGGGGACACCTTGTCTCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCTTGGCAAC 360
Qy 121 SerLeuMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCCATCATGTACTTTCAGCCACTTCTGTCGGCTTCTCCGCAAGAGTTGGGGACACCTTGTCTCTC 420
```

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCCCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGCGCTGCGCGCCAGCGCGGGGGGCGAGTCACACGAGGGGGTGACTTCGCC 540
QY 171 ----- 171
Db 541 TGTGATATCTACATCTGGGGCGCTTGGCGGGACTTGTGGGTCTCTCTGTCTACATG 600
QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCCTTACTGCAACACACAGGAACCGAGACGTGTTGCAAAATGTCCCCGGCCT 660
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 661 GTGGTCAATCGGGAGACAGCCAGCCCTTTGGCGAGATACGTC 705
RESULT 8
ADS19462
ID ADS19462 standard; DNA; 708 BP.
XX
AC ADS19462;
XX
DT 16-DEC-2004 (first entry)
XX
DE Coding sequence DNA of the human CD8 alpha chain mRNA.
KW gene; de; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..708
FT /*tag= a
FT /product= "CD8 alpha chain protein"
XX
XX WO2004083404-A2.
XX
XX 30-SEP-2004.
XX
XX 19-MAR-2004; 2004WO-US008567.
XX
XX 19-MAR-2003; 2003US-0456378P.
XX
XX (ISOG-) ISOGENIS INC.
XX
XX Qi Y, Zhang X, Konigsberg PJ;
XX
XX WPI; 2004-691049/67.
XX
XX P-PSDB; ADS19436.
XX
PT New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
PT operably linked to a nucleic acid encoding a transmembrane polypeptide,
PT useful for inhibiting cellular and humoral components of the host immune
PT responses.
XX
PS Disclosure; Fig 2a; 94pp; English.
XX
XX This invention relates to novel gene therapy vectors with reduced
XX immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
XX alpha chain operably linked to nucleic acid encoding a transmembrane
XX polypeptide and a second nucleic acid representing the therapeutic gene
XX of interest (for example ornithine carbamoyl transferase or beta
XX glucosidase), whereby transcriptional and translational control elements
XX direct expression thereof. The present invention describes a method to
XX reduce an immune response against antigens derived from a gene therapy
XX delivery system i.e. improving the expression of a therapeutic transgene
XX in a host and improving viral expression vectors with reduced
XX immunogenicity. Accordingly, these compositions are useful for inhibiting

CC both the cellular and humoral components of the host immune responses
CC against expression vectors and target cells transfected with the vectors.
CC As such, they exhibit immunosuppressive activity, this polynucleotide is
CC the coding sequence DNA of the human CD8 alpha chain mRNA of the
CC invention.
XX
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-65 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 13 Gaps: 1

US-10-804-763-3 (1-198) x ADS19462 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCTTACCAGTGACCGCCTTGTCTCGCGCTGGCCTTGTCTCCACGCGCCAGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTGCCAGGTGCTGTCTCAACCCGACGTCGGGTGTCTGTGGTCTTCTCCAGCCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCCAGTCCACCTTCTCTCTATATCTCTCCAAAAACAAGCCCAAGGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGCGAAGAGTTGGGGACACCTTCTGCTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCGGCCCTTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGGCACCTTCGTGCGGTCTTCTCGCAGCGAAGCCACACGACG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCCGAGCCCTGTCCCTGCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGCGCTGCGCGCCAGCGCGGGGGGCGAGTCACACGAGGGGGTGACTTCGCC 540
QY 171 ----- 171
Db 541 TGTGATATCTACATCTGGGGCGCTTGGCGGGACTTGTGGGTCTCTCTGTCTACATG 600
QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCCTTACTGCAACACACAGGAACCGAGACGTGTTGCAAAATGTCCCCGGCCT 660
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 661 GTGGTCAATCGGGAGACAGCCAGCCCTTTGGCGAGATACGTC 705
RESULT 9
ADV42461
ID ADV42461 standard; cDNA; 708 BP.
XX
AC ADV42461;
XX
DT 10-MAR-2005 (first entry)

XX DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 89.
 KW microarray; psychoneuroendocrinimmune; chronic fatigue;
 KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
 KW cancer; neoplasm; infection; expressed sequence tag; ss.
 XX Homo sapiens.
 OS
 XX WO2004108899-A2.
 XX 16-DEC-2004.
 XX 04-JUN-2004; 2004WO-US017686.
 XX 04-JUN-2003; 2003US-0475915P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Nicholson A, Vernon SD;
 XX WPI; 2005-031682/03.
 XX New microarray comprising probes for genes involved in
 PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
 PT condition associated with PNI activity, e.g., inflammatory or infectious
 PT diseases.
 XX Claim 1; SEQ ID NO 89; 254pp; English.
 XX The invention relates to a new microarray which comprises probes for
 CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
 CC microarray is useful in diagnosing a condition associated with PNI
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 CC cancer and infection. The present sequence represents a
 CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
 CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
 CC SEQ ID NO 1829 are provided.
 XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,55e-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservative: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 14 Gaps: 1

US-10-804-763-3 (1-198) x ADV42461 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 Db 1 ATGGCTTACAGTGACCGCTTGCTCTCGCGCTGGCTTGCTGCTCCACGCCGCCAGG 60
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 61 CCGAGCCAGTTCGGGTGTCGGCTGGTGGACCTGGACCTGGCGGAGACAGTGGAG 120
 Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpPheGlnPro 60
 Db 121 CTGAAGTCCAGGTGCTGTGTCACCGAGCTGGGTGCTGCTGCTCTTCCAGCGG 180
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 Db 181 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGG 240
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 241 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 300
 Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120

Db 301 ACCGTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 361 TCCATCATGTACTTACGCCACTTCGTGCGGTCTTCTGCGCGAAGCCCAACGACG 420
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 421 CCAGCGCGGACCAACCAACCGCGGCCCAACCATCGCTCGCAGCCCTGTCCCTGCGC 480
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 481 CCAGAGCGGTGCCGCGCAGCGCGGGGGGCGCAGTGCACACGAGGGGCTGGACTTCGCC 540
 Qy 171 ----- 171
 Db 541 TGTGATATCTACATCTGGGGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTGCACTG 600
 Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
 Db 601 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAATGTCCCGGCT 660
 Qy 184 ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 661 GTGGTCAATCGGAGACACAGCCCGCTTTCGGCGAGATACGTC 705

RESULT 10
 AEF68357
 ID AEF68357 standard; cDNA; 708 BP.
 XX AEF68357;
 AC AEF68357;
 XX 06-APR-2006 (first entry)
 DT
 XX Human CD8 alpha chain cDNA.
 DE
 XX immune inhibition; CD8; spinal cord injury; neuroprotective; vulnery;
 KW autoimmune disease; immunosuppressive; immune disorder; diabetes;
 KW antidiabetic; endocrine disease; gastrointestinal disease;
 KW metabolic disorder; uveitis; antiinflammatory; ophthalmological;
 KW inflammation; cirrhosis; hepatotropic; gastrointestinal disease;
 KW neurodegenerative disease; neuroprotective; neurological disease;
 KW osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease;
 KW obesity; anorectic; nutritional disorder; ss; gene.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..708
 FT CDS
 FT /*tag= b
 FT /product= "CD8 alpha chain"
 FT /transl_except= (pos:67..69,aa:Gly)
 FT /transl_except= (pos:130..132,aa:Gly)
 FT /transl_except= (pos:175..177,aa:Gly)
 FT /transl_except= (pos:223..225,aa:Gly)
 FT /transl_except= (pos:259..261,aa:Gly)
 FT /transl_except= (pos:463..465,aa:Gly)
 FT sig_peptide 1..63
 FT /*tag= a
 FT mat_peptide 64..705
 FT /*tag= c
 FT /product= "Mature CD8 alpha chain"
 XX WO2006012416-A2.
 PN
 XX 02-FEB-2006.
 PD
 XX 20-JUL-2005; 2005WO-US025878.
 PF
 XX 20-JUL-2004; 2004US-0589707P.
 PR 29-SEP-2004; 2004US-0614529P.
 XX (ISOG-) ISOGENIS INC.
 PA

XX Qi Y, Staerz UD;
 XX WPI: 2006-125925/13.
 DR P-PSDB; AEF68356.
 XX
 PT New composition comprising CD8 polypeptide and autoantigen protein,
 PT useful for preventing or treating autoimmune disease, diabetes,
 PT neurodegenerative diseases, osteoarthritis.
 XX
 PS Disclosure; Fig 1A; 85pp; English.
 XX
 CC The invention relates to a therapeutic composition for inhibiting an
 CC autoreactive T cell response, comprising an expression vector encoding a
 CC CD8 polypeptide and an autoantigen protein or its fragment, or at least
 CC one epitope of an autoantigen associated with the autoreactive T cell
 CC response. Also described are: (1) a polynucleotide comprising a first
 CC nucleic acid sequence encoding a CD8 polypeptide, a second nucleic acid
 CC sequence encoding at least one epitope of an autoantigen associated with
 CC an autoreactive T cell response, and control sequences operably linked
 CC with the first and second nucleic acids for expression in a target cell;
 CC (2) a method for inhibiting an autoimmune response to a target antigen;
 CC and (3) a method of preventing the development of or for treating an
 CC autoimmune disease in a host. The composition and methods are useful for
 CC inhibiting an autoimmune response to a target antigen, and for preventing
 CC the development of or for treating autoimmune disease, diabetes, uveitis,
 CC cirrhosis, neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Huntington's disease, or Parkinson's disease), osteoarthritis, obesity,
 CC or spinal cord injury. The present sequence represents human CD8 alpha
 CC chain cDNA.
 XX
 SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,55e-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservative: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 15 Gaps: 1

US-10-804-763-3 (1-198) x AEF68357 (1-708)

QY 1 MetaLaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 DB 1 ATGGCTTTACAGTACCGCCTTGCTCTCGCGCTGGCTTCTGCTTCCACGCCCGCAGG 60
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 DB 61 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 120
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 DB 121 CTGAAGTCCAGGTGCTGCTGCCAACCGACGTGGGTGCTGCTGGGTCTTTCAGCGG 180
 QY 61 ArgGlyAlaAlaAsaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 DB 181 CGGCGCGCGCGCGCCAGTCCCACTTCTCTATACCTTCTCCAAAACAGCCCAAGCGG 240
 QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 DB 241 GCGGAGGGGCTGGACACCCAGCGGTTCGCGCAAGAGTTGGGGGACACCTTCGTCCTC 300
 QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
 DB 301 ACCCTGAGCGACTCCCGCGAGAACGAGGGCTACTATTTCTGTCGGCGCTTGAGCAAC 360
 QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 DB 361 TCCATCATGTAATTCAGGCACCTTCGTCGGGTCTTCTGCCAGCGAAGCCACACGACG 420
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

DB 421 CCAGCGCGCGGACACCAACACCGGGGCCCATCATCGCGTGCAGGCCCTGTCCCTGGCG 480
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 DB 481 CCAGAGGGCGTCCGCCAGCGCGGGGGCGCAGTGTCACACGAGGGGGCTGGACTTCGCC 540
 QY 171 ----- 171
 DB 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGGAGCTTGTGGGGTCTCTCTCTGCTCACTG 600
 QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 193
 DB 601 GTTATCACCTTTACTGCAACACACAGGACCGAAGACGTGTTGCAAAATGTCCCGCCT 660
 QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 DB 661 GTGGTCAATCGGGAGACCAAGCCCTTTCGGCGAGATACGTC 705

RESULT 11
 AAQ57986
 ID AAQ57986 standard; DNA; 1060 BP.
 AC AAQ57986;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-AUG-1994 (first entry)
 XX
 DE Genomic sequence of human CD8.
 XX
 KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;
 KW fusion protein; CD8; fusion protein; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 66..773
 FT /*tag= a
 XX
 PN EP585943-A2.
 XX
 PD 09-MAR-1994.
 XX
 PF 03-SEP-1993; 93EP-00114153.
 PR 04-SEP-1992; 92US-00940605.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Aruffo A, Hollenbaugh D, Ledbetter JA;
 XX
 DR WPI; 1994-076264/10.
 DR P-PSDB; AAR59550.
 XX
 PT New nucleic acid encoding human gp39 T cell antigen - which is a ligand
 PT for the CD40 receptor, causing proliferation and differentiation of B
 PT cells and some cancer cells.
 XX
 PS Disclosure; Fig 9; 39pp; English.
 XX
 CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in
 CC AAQ57984 and AAR49548 respectively and contd. in plasmid CDMS-hgp39,
 CC deposited with the ATCC as E. coli, CDMS MC1061/p3-hgp39 and assigned
 CC accession No. 69050. The human T cell antigen gp39 is a ligand for the
 CC CD40 receptor. Soluble gp39 may be produced using the expression vector
 CC CD8-gp39. Chimeric genes may be constructed by fusing sequences encoding
 CC the extracellular domains of gp39 and CD8, pref. murine or human CD8
 CC protein, plasmid p3-shgp39 encoding the fusion protein of the
 CC extracellular domains from gp39 and CD8 is deposited in E.coli as ATCC
 CC 69049. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.02e-65 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x AAQ57986 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiaAlaAarg 20
DB 66 ATGGCCTTACAGTGACCGCCTTGTCTCGCGCTTGGCTTGTCTCCAGCGCCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 126 CCGAGCCAGTTCGGGTGCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 246 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGC 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 366 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTCGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 426 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCGCAGCGAAGCCACACGACG 485
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCAGCGCGCGACCAACACCGCGCGCGCGCAGTCAGTCACAGAGGGGCTCGACTTCGCC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 546 CCAGAGGCGTGCAGCG 605
QY 171 ----- 171
DB 606 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCACTG 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 666 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAATGTCCTCCGCGCT 725
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
DB 726 GTGGTCAAAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 770

RESULT 12

ADD25612

ID ADD25612 standard; DNA; 1060 BP.

XX AC

XX AC

XX ADD25612;

DT 15-JAN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated DNA #90.

XX ds; Binding domain; immunoglobulin; fusion protein; cytostatic;

KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;

KW neuroprotective; hinge region; immunoglobulin heavy chain;

KW CH2 constant region; CH3 constant region; IgG1;

KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;

KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX type I diabetes mellitus; multiple sclerosis; autoimmune disease.
OS Unidentified.
XX US2003118592-A1.
PN 26-JUN-2003.
XX 25-JUL-2002; 2002US-00207655.
PF 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX (GENE-) GENE-CRAFT INC.
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
FI WPI; 2003-801317/75.
DR PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX Disclosure; SEQ ID NO 173; 157pp; English.
PS Unidentified
XX SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;
XX Alignment Scores:
Pred. No.: 4.02e-65 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1
US-10-804-763-3 (1-198) x ADD25612 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiaAlaAarg 20
DB 66 ATGGCCTTACAGTGACCGCCTTGTCTCGCGCTTGGCTTGTCTCCAGCGCCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 126 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 246 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGC 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGTGGACACCCAGCGGTCTTCGGCGAAGAGTTGGGGGACACCTTCGTCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 366 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTCGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 426 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCGCAGCGAAGCCACACGACG 485
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCAGCGCGCGACCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545

The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray can be used in the diagnosis of an immunopathology, such as Crohn's disease, asthma,

ID ADS83755 standard; cDNA; 1060 BP.
 AC ADS83755;
 XX
 DT 11-AUG-2005 (first entry)
 DE Human lymph node cDNA #1014.
 XX
 XX ss; gene; human; immunological response; blood cell; cancer;
 KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
 KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
 KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
 XX
 OS Homo sapiens.
 XX
 PN US2004077003-A1.
 XX
 XX 22-APR-2004.
 XX
 XX 14-AUG-2003; 2003US-00641643.
 PF
 XX 09-FEB-1998; 98US-00023655.
 XX
 XX (INCY-) INCYTE CORP.
 PA
 XX Cocks BG, Stuart SG, Seilhamer JJ;
 XX
 XX WPI; 2004-387937/36.
 DR
 XX
 XX New compositions having a number of first, second and third
 PT polynucleotide probes, useful in research and diagnostic applications in
 PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
 PT infections.
 XX
 XX Claim 15; SEQ ID NO 1014; 16pp; English.
 PS
 XX The invention relates to polynucleotides which are used as probes to
 CC detect genes differentially expressed in an immunological response,
 CC abundantly expressed in an immunological response and/or coding for a
 CC polypeptide known to regulate blood cell biology. The polynucleotides are
 CC useful in research and diagnostic applications particularly in cancer and
 CC immunopathological conditions, such as AIDS, allergies, asthma,
 CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
 CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
 CC present sequence represents a human lymph node cDNA used to detect blood
 CC cell and immunological response gene expression. Note: The present
 CC sequence does not appear in the printed specification but was obtained in
 CC electronic format from the USPTO web site
 CC (seqdata.uspto.gov/sequence.html?docID=20040077003).
 XX
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 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
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 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
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 Qy 171 ----- 171
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RESULT 15
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 ID ADF90782 standard; DNA; 2123 BP.
 AC ADF90782;
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 DT 26-FEB-2004 (first entry)
 DE Human hepatic-fibrosis disease marker SEQ ID 244.
 XX
 KW Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 KW hepatic carcinoma; human; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP2003259877-A.
 XX
 PD 16-SEP-2003.
 XX
 PF 11-MAR-2002; 2002JP-00065013.
 XX
 PR 11-MAR-2002; 2002JP-00065013.
 XX
 XX (SUMU) SUMITOMO SEIYAKU KK.
 XX
 XX WPI; 2003-821598/77.
 XX
 PT Hepatic fibrosis disease markers comprising polynucleotides or
 PT antibodies, useful for improved diagnosis, screening and developing drugs
 PT to treat hepatitis, to control cirrhosis and carcinoma.
 XX
 PS Claim 1; SEQ ID NO 244; 313pp; Japanese.
 XX
 CC The present invention relates to hepatic-fibrosis disease markers
 CC (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The
 CC sequences are useful for detecting and treating hepatic fibrosis caused

CC by alcohol consumption, virus infection, etc., and the associated chronic
 CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
 CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
 precision), so more suitable treatments can be developed and given.
 XX

SQ Sequence 2123 BP; 508 A; 586 C; 528 G; 501 T; 0 U; 0 Other;

Alignment Scores:

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 Score: 1006.50 Matches: 197
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US-10-804-763-3 (1-198) x ADF90782 (1-2123)

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| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
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 Job time : 768.277 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 29, 2006, 11:19:03 ; Search time 212.633 Seconds
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Title: US-10-804-763-3

Perfect score: 1043

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 1006.5 | 96.5 | 1060 | 3 | US-09-023-655-1014 Sequence 1014, Ap |
| 4 | 997.5 | 95.6 | 2150 | 5 | US-10-131-831-9109 Sequence 9109, Ap |
| 5 | 899 | 86.2 | 1131 | 3 | US-08-751-512-7 Sequence 7, Appl |
| 6 | 623 | 59.7 | 822 | 2 | US-08-403-853-11 Sequence 11, Appl |
| 7 | 352.5 | 33.8 | 803 | 3 | US-09-477-737-2 Sequence 2, Appl |
| 8 | 352.5 | 33.8 | 972 | 2 | US-07-940-605A-9 Sequence 9, Appl |

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| 9 | 352.5 | 33.8 | 972 | 2 | US-08-690-096-9 | Sequence 9, Appl |
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| 14 | 136 | 13.0 | 5526 | 3 | US-08-751-359-21 | Sequence 21, Appl |
| 15 | 136 | 13.0 | 5526 | 2 | US-08-907-146-21 | Sequence 21, Appl |
| 16 | 135 | 12.9 | 1202 | 3 | US-08-491-988-27 | Sequence 27, Appl |
| 17 | 132 | 12.7 | 1178 | 2 | US-08-491-988-28 | Sequence 28, Appl |
| 18 | 132 | 12.7 | 1235 | 2 | US-08-491-988-11 | Sequence 11, Appl |
| 19 | 131.5 | 12.6 | 1259 | 3 | US-08-491-988-24 | Sequence 24, Appl |
| 20 | 129 | 12.4 | 315 | 2 | US-10-083-424-31 | Sequence 31, Appl |
| 21 | 128.5 | 12.3 | 927 | 2 | US-07-690-192-1 | Sequence 1, Appl |
| 22 | 127.5 | 12.2 | 1295 | 2 | US-08-491-988-26 | Sequence 26, Appl |
| 23 | 127 | 12.2 | 723 | 7 | PCT-US94-14106-60 | Sequence 60, Appl |
| 24 | 127 | 12.2 | 1178 | 2 | US-08-491-988-25 | Sequence 25, Appl |
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| 26 | 125 | 12.0 | 805 | 3 | US-09-620-312D-62 | Sequence 62, Appl |
| 27 | 125 | 12.0 | 1174 | 3 | US-09-949-002-216 | Sequence 216, App |
| 28 | 125 | 12.0 | 1192 | 3 | US-09-949-002-89 | Sequence 89, Appl |
| 29 | 125 | 12.0 | 103947 | 3 | US-09-949-002-788 | Sequence 788, App |
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| 31 | 124.5 | 11.9 | 431 | 2 | US-08-345-321-7 | Sequence 7, Appl |
| 32 | 124.5 | 11.9 | 915 | 4 | US-09-880-107-3743 | Sequence 3743, Ap |
| 33 | 124 | 11.9 | 1632 | 2 | US-08-792-824-8 | Sequence 8, Appl |
| 34 | 124 | 11.9 | 1641 | 2 | US-08-792-824-5 | Sequence 5, Appl |
| 35 | 124 | 11.9 | 1644 | 2 | US-08-792-824-11 | Sequence 11, Appl |
| 36 | 124 | 11.9 | 1672 | 2 | US-08-792-824-2 | Sequence 2, Appl |
| 37 | 124 | 11.9 | 4435 | 2 | US-08-792-824-1 | Sequence 1, Appl |
| 38 | 123.5 | 11.8 | 420 | 10 | 5219996-18 | Patent No. 5219996 |
| 39 | 123.5 | 11.8 | 891 | 3 | US-09-049-672A-23 | Sequence 23, Appl |
| 40 | 123.5 | 11.8 | 1624 | 2 | US-08-491-988-14 | Sequence 14, Appl |
| 41 | 123 | 11.8 | 938 | 3 | US-09-828-995B-25 | Sequence 25, Appl |
| 42 | 123 | 11.8 | 938 | 3 | US-09-828-995B-27 | Sequence 27, Appl |
| 43 | 122.5 | 11.7 | 1143 | 3 | US-09-700-820C-27 | Sequence 27, Appl |
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| 45 | 122.5 | 11.7 | 1611 | 3 | US-09-968-851A-37 | Sequence 37, Appl |

ALIGNMENTS

RESULT 1
US-07-940-605A-11
; Sequence 11, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090

NC

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; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-940-605A-11

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Pred. No.: 3.14e-76 Length: 1060
Score: 1006.50 Matches: 197
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Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x US-07-940-605A-11 (1-1060)

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; Sequence 11, Application US/08690096
; Patent No. 5945513
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US-09-023-655-1014
; Sequence 1014, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: g179145
US-09-023-655-1014
Alignment Scores:
Pred. No.: 3,14e-76 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 3 Gaps: 1

US-10-804-763-3 (1-198) x US-09-023-655-1014 (1-1060)

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RESULT 4

US-10-131-831-9109
; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121

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; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Alignment Scores:
Pred. No.: 4,56e-75 Length: 2150
Score: 997.50 Matches: 196
Percent Similarity: 83.4% Conservative: 0
Best Local Similarity: 83.4% Mismatches: 2
Query Match: 95.6% Indels: 37
DB: 5 Gaps: 1

US-10-804-763-3 (1-198) x US-10-131-831-9109 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6 ATGGCTTACAGTACGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCCAGG 65

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 66 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 125

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGTGGCTCTTCAGCGC 185

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGCGCGCGCGCGACGCCACCTTCTCTATACCTCTCCCAAAAACAAGCCAAAGCG 245

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 246 GCCGAGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTGGGGGACACCTTCGTCTC 305

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 306 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTGCTATTTCTGCTCGGCTTGAGCAAC 365

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 366 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCGAAGCCCAACGACG 425

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 426 CCAGCGCGCGACCAACCAACCGCGGCCACCATCGCGTGCAGCCCTGTCCCTGCGC 485

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 486 CCAGAGGCGTGC CGGCCAGCGCGGGGGCGCGAGTGCACAGAGGGGCTGGACTTCGCC 545

Qy 171 ----- 171
Db 546 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCCTTCTCTGTCACTG 605

Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 606 GTTATCACCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAATGTCCCGGCT 665

Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 666 GTGGTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 710

US-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramer, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified FAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1128
US-08-751-512-7

Alignment Scores:
Pred. No.: 4.31e-67 Length: 1131
Score: 899.00 Matches: 172
Percent Similarity: 98.9% Conservative: 1
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 86.2% Indels: 0
DB: 3 Gaps: 0

US-10-804-763-3 (1-198) x US-08-751-512-7 (1-1131)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACAGTACGACCGCTTGTCTCGCGCTGGCTTGTCTCTCCACGCCGCCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGTGGCTCTTTCAGCGC 180

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAAACAAGCCAAAGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGCTGGACACCCAGCGGTTCCTCGGCGAAGAGTGGGGGACACCTTCGTCTC 300

RESULT 5
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QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCAGAGAAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCATCATGTACTTCAGCCACATTCGTGCGCGGTCTTCTGCGCAGGAAGCCACCGACG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGACGCCCTGTCTCCCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArg 175
Db 481 CCAGAGCGCTGCGCGCAGCGCGGGGGCGGCGCAGTGCACACGAGG 525

RESULT 6

US-08-403-853-11
; Sequence 11, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara B.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..819
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..819

US-08-403-853-11

Alignment Scores:
Pred. No.: 6,6e-44 Length: 822
Score: 623.00 Matches: 124
Percent Similarity: 94.0% Conservative: 1
Best Local Similarity: 93.2% Mismatches: 6
Query Match: 59.7% Indels: 6
DB: 2 Gaps: 2

US-10-804-763-3 (1-198) x US-08-403-853-11 (1-822)

QY 9 LeuLeuProLeuAla-----LeuLeuLeuHisAlaAlaArgPro-----Ser 22
Db 10 CTATTGCTTACGCGAGCGCGCTGGATTGTTATTACTGCTGCGCAACACCGATGGCCAGC 69
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 70 CAGTTCCGGGTGTCGCGCTGGATCGGACCTCGGAACCTGGCGGAGACAGTGGAGCTGAAG 129
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 130 TGCCAGGTGCTGCTGTCCAACCCGAGCTCGGGCTGCTGCTGCTCTTCCAGCGCGCGGC 189
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 190 GCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGCGCGAG 249
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 250 GGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGAGACACCTTCCTCACCCTG 309
QY 103 SerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db 310 AGCGACTTCCCGCGAGAGAACGAGGCTACTATTCTGCTGCGCCCTGAGCAACTCCATC 369
QY 123 MetTyrPheSerHisPheValProValPheLeuProAla 135
Db 370 ATGTACTTCAGCCACTTCGTGCGCGGTCTTCTGCGCAGCG 408

RESULT 7

US-09-477-737-2
; Sequence 2, Application US/09477737
; Patent No. 6544506
; GENERAL INFORMATION:
; APPLICANT: Reiser
; TITLE OF INVENTION: VETO CELLS EFFECTIVE IN PREVENTING GRAFT REJECTION AND DEVOID O.
; TITLE OF INVENTION: VERSUS HOST POTENTIAL
; FILE REFERENCE: 00/20548
; CURRENT APPLICATION NUMBER: US/09/477,737
; CURRENT FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-477-737-2

Alignment Scores:
Pred. No.: 5,08e-21 Length: 803
Score: 352.50 Matches: 96
Percent Similarity: 51.6% Conservative: 33
Best Local Similarity: 38.4% Mismatches: 66
Query Match: 33.8% Indels: 55
DB: 3 Gaps: 13

US-10-804-763-3 (1-198) x US-09-477-737-2 (1-803)

QY .1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 13 ATGGCCCTCACCGTTGACCGCTTCTGCTGCTGAACCTGCTGCTGCTGGTGAGTCGATT 72

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Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 73 ATCTGTGGAGTGGAGAACTAAAGCCACAGCCAGCCGAACTCCGAATCTTCCAAAGAAA 132
Qy 31 ArgThrTrpAenLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 133 ATGACGCCGCAACTGGTCAGAAAGTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 189
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 190 TCGCAAGAGTCTCTTGGCTCTTCAGAACTCCAGCTCCAACTCCCCAGCCACCTTC 249
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 250 GTTGCTATATGGCTTCTATCCCAACAAGATAACGTGGGACGAGAACTGAATTCGTCG 309
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 310 AAACGTGTTTCTGCATCAGGACGACGACGAAATAATAGTACGTCTCACCCTGACAAAGTTC 369
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 370 AGCAAGGAAAACGAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 429
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 430 AGTTCTGTGCGCCAGCTCTTCAGAAAGTGAACTCTACTACTACCAAGCCAGTGTGCGGA 489
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 490 ACTCCTCACCCTGTCACCTACCGGACATCTCAGCCC-----CAGAGACCAGAGAT 543
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGly----- 172
Db 544 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGATTGGACTTCGCCTGTGATATTACATC 603
Qy 172 ----- 172
Db 604 TGGGACCCCTTGGCGGAAATCTGGTGCCCTTCTGCTGCTGATCATCTCTCATC 663
Qy 173 -----AsnArgArgValCysLysCysProArgProValValLysSerGly 188
Db 664 TGCTACCACAGGACCGGAAAGGCTTTGCAAAATGTCACAGCCGCTAGTCAGACAGGAA 723
Qy 189 AspLysProSerLeuSerAlaArgTyrVal 198
Db 724 GGCAGGCCAGACCTTTCAGAGAAAATTTGTG 753
```

RESULT 8

US-07-940-605A-9
; Sequence 9, Application US/07940605A
; Patent No. 5540926

GENERAL INFORMATION:

; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992

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; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 972 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-940-605A-9  
  
Alignment Scores: 6.51e-21 Length: 972  
Pred. No.: 352.50 Matches: 96  
Score: 51.6% Conservative: 33  
Percent Similarity: 38.4% Mismatches: 66  
Best Local Similarity: 33.8% Indels: 55  
Query Match: 2 Gaps: 13  
DB: 13  
  
US-10-804-763-3 (1-198) x US-07-940-605A-9 (1-972)  
  
Qy 1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14  
Db 127 ATGCGCTCACCGTTGACCGCTTTCTGTCGTGAACCTGCTGCTGGTGAGTCGATT 186  
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30  
Db 187 ATCTGGGGAGTGAGAAAGCTTAAGCCACAGCACCCGAACTCCGAATCTTCCAAAGAAA 246  
Qy 31 ArgThrTrpAenLeuGlyGluThrValGluLeuLysCysGlnValLeuSerAsnPro 50  
Db 247 ATGACGCCGCAACTGGTCAGAAAGTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 303  
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69  
Db 304 TCGCAAGAGTCTCTTGGCTCTTCAGAACTCCAGCTCCAACTCCCCAGCCACCTTC 363  
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87  
Db 364 GTTGCTATATGGCTTCTATCCCAACAAGATAACGTGGGACGAGAAAGCTGAATTCGTCG 423  
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105  
Db 424 AAACGTGTTTCTGCATGAGGACACGAAATAATAGTACGTCTCACCCTGAAACAGTTC 483  
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125  
Db 484 AGCAAGGAAAACGAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543  
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144  
Db 544 AGTTCTGTGCGCCAGCTCTTCAGAAAGTGAACTCTACTACTACCAAGCCAGTGTGCGGA 603  
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163  
Db 604 ACTCCTCACCCTGTCACCTACCGGACATCTCAGCCC-----CAGAGACCAGAGAT 657  
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGly----- 172  
Db 658 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGATTGGACTTCGCCTGTGATATTACATC 717  
Qy 172 ----- 172  
Db 718 TGGGACCCCTTGGCGGAAATCTGGTGCCCTTCTGCTGCTGATCATCATCTCTCATC 777  
Qy 173 -----AsnArgArgValCysLysCysProArgProValValLysSerGly 188
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Query Match: 29.8% Indels: 22
DB: 3 Gaps: 12

US-10-804-763-3 (1-198) x US-09-966-976A-8 (1-8345)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 4974 ATGCGCTCACCGTTGACCGCGTTTCTGTCGCTGAACCTGCTGCTGGTGAGTCGATT 4915
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 4914 ATCTGGGGAGTGAGGAAGCTTAAGCCACAGCAGCCAGCACTCCGAATCTTTCCAAAGAAA 4855
Qy 31 ArgThrTrpAsnLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 4854 ATGACGCCGGAACCTGGTCAGAGGTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 4798
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 4797 TCGCAAGGATGCTCTTGCTCTCCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 4738
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 4737 GTTGTCTATATGGCTTCTATCCACACAAAGATAACGTGGGACGAGAACTGAATTCGTCG 4678
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 4677 AAACGTGTTTCTGCCATGAGGACACGAAATAAAGTACGTTCTCACCTGAACAAGTTC 4618
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 4617 AGCAAGGAAACGAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 4558
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThr---ProAlaProArg 144
Db 4557 AGTTCTGTCGTCGCGAGGCTCTTCCAGAAAGTGAACCTACTACTACCAAGCCAGTGTGCGA 4498
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 4497 ACTCCCTCACCTGTGCACCTACCGGACATCTCAGCCC-----CAGAGACCAAGAT 4444
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGlyAsnArg 174
Db 4443 TGTGCGCCCGTGGTCTCAGTGAAGGGACCGGAAACCGG 4405

RESULT 11
US-09-076-624-8/c
; Sequence 8, Application US/09076624A
; Patent No. 7001733
; GENERAL INFORMATION:
; APPLICANT: FERRICK et al.
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators
; TITLE OF INVENTION: and Ige Synthesis, Secretion and Switch Rearrangement
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/076,624A
; CURRENT FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-076-624-8

Alignment Scores:
Pred. No.: 3,48e-16 Length: 8345
Score: 311.00 Matches: 84
Percent Similarity: 58.0% Conservative: 28
Best Local Similarity: 43.5% Mismatches: 59
Query Match: 29.8% Indels: 22
DB: 5 Gaps: 12

US-10-804-763-3 (1-198) x US-09-076-624-8 (1-8345)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 4974 ATGCGCTCACCGTTGACCGCGTTTCTGTCGCTGAACCTGCTGCTGGTGAGTCGATT 4915
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 4914 ATCTGGGGAGTGAGGAAGCTTAAGCCACAGCAGCCAGCACTCCGAATCTTTCCAAAGAAA 4855
Qy 31 ArgThrTrpAsnLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 4854 ATGACGCCGGAACCTGGTCAGAGGTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 4798
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 4797 TCGCAAGGATGCTCTTGCTCTCCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 4738
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 4737 GTTGTCTATATGGCTTCTATCCACACAAAGATAACGTGGGACGAGAACTGAATTCGTCG 4678
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 4677 AAACGTGTTTCTGCCATGAGGACACGAAATAAAGTACGTTCTCACCTGAACAAGTTC 4618
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 4617 AGCAAGGAAACGAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 4558
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThr---ProAlaProArg 144
Db 4557 AGTTCTGTCGTCGCGAGGCTCTTCCAGAAAGTGAACCTACTACTACCAAGCCAGTGTGCGA 4498
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 4497 ACTCCCTCACCTGTGCACCTACCGGACATCTCAGCCC-----CAGAGACCAAGAT 4444
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGlyAsnArg 174
Db 4443 TGTGCGCCCGTGGTCTCAGTGAAGGGACCGGAAACCGG 4405

RESULT 12
US-08-403-853-9
; Sequence 9, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..840
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..840
US-08-403-853-9

Alignment Scores:
Pred. No.: 8,888-13 Length: 849
Score: 255.50 Matches: 80
Percent Similarity: 51.9% Conservative: 30
Best Local Similarity: 37.7% Mismatches: 70
Query Match: 24.5% Indels: 32
DB: 2 Gaps: 11

US-10-804-763-3 (1-198) x US-08-403-853-9 (1-849)
QY 9 LeuLeuProLeuAla-----LeuLeuLeuHisAlaAlaArgProSer----- 22
Db 10 CTATTGCTTACGCGAGCGCTGGATTGTTATTCTCGCTGCCCAACGAGCGGCGCAAG 69

QY 23 -----GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThr 38
Db 70 CCACAGGACCCGGAACCTCGAATCTTCCAAAGAAATGACGCCGGAACCTTGGTCAGAAG 129

QY 39 ValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPhe 58
Db 130 GTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTTTCGCAAGGATGCTCTTGGCTCTTC 186

QY 59 GlnProArgGlyAla---AlaAlaSerProThrPheLeuLeuTyrrLeu-----SerGln 75
Db 187 CAGAACTCGAGTCCAAACTCCCGAGCCACCTTCGTGTCTATATGCTTCATCCAC 246

QY 76 AsnLysProLysAlaAlaGluGlyLeuAspThrGlnArg---PheSerGlyLysArg--- 93
Db 247 AACAGATAACCTGGGACGAGAGCTGAATTCGTGMAACTGTTTCTGCCATGAGGAC 306

QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrr 113
Db 307 ACGATAATAAGTACGTTCTACCCCTGAACAGTTTCAGCAAGAAACGAGGCTACTAT 366

QY 114 PheCysSerAlaLeuSerAsnSerileMetTyrrPheSerHisPheValProVal-PheLe 133
Db 367 TTCTCTCAGTCATCAGCAACTCGGGTGATGTAATCTCAGTTCTGTCGTCAGTCTCTCAG 426

QY 133 uProAlaLysProThrThrPro-----AlaProArgProPr 146
Db 427 GGTGGCGGAGGCTCAGGCGGTGGTGGATCAGTGGCGGCGGATCTCTCATTCAGACCCCT 486

QY 146 oThrProAla-----ProThrIleAlaSerGln---ProLeuSerLeuArgProGl 162
Db 146 oThrProAla-----ProThrIleAlaSerGln---ProLeuSerLeuArgProGl 162

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Db 487 TCGTCCCTGCTGTTTCAAAACCAACCATACGCAAGATGTCCTGTGAGGTAAAGCATC 546
QY 162 uAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCysProAr 182
Db 547 TCTAAGTTAACAGCATCTACTGGCTGCGGAGGCCAGG-----ACCCCAAG 594
QY 182 gProValVallysSerGlyAspLysProSerLeu 193
Db 595 GACAAGTACTTTGAGTTCCTCGCTCTCTGGAGTT 628

RESULT 13
US-09-596-774-5
; Sequence 5, Application US/09596774
; Patent No. 6984382
; GENERAL INFORMATION:
; APPLICANT: GRONER, BERND
; APPLICANT: MORITZ, DIRK
; TITLE OF INVENTION: BIFUNCTIONAL PROTEIN, PREPARATION AND USE
; FILE REFERENCE: 24741-1521
; CURRENT APPLICATION NUMBER: US/09/596,774
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/159,027
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 08/793,048
; PRIOR FILING DATE: 1996-11-01
; PRIOR APPLICATION NUMBER: PCT/EP95/01494
; PRIOR FILING DATE: 1995-04-20
; PRIOR APPLICATION NUMBER: EP 94810244.7
; PRIOR FILING DATE: 1994-05-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 5
; TYPE: DNA
; LENGTH: 1479
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: chimeric nucleotide sequence
; NAME/KEY: CDS
; LOCATION: (40)..(1422)
US-09-596-774-5

Alignment Scores:
Pred. No.: 1,088-05 Length: 1479
Score: 175.50 Matches: 58
Percent Similarity: 42.3% Conservative: 24
Best Local Similarity: 29.9% Mismatches: 77
Query Match: 16.8% Indels: 36
DB: 4 Gaps: 8

US-10-804-763-3 (1-198) x US-09-596-774-5 (1-1479)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 449 CTGGCGGTGGCGGTCTCTGGTGGCGGTGCTCGCGGTGCTCGACATCCAGCTGA 508
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 509 CCCAGTCTCAAAATCTCTGCTCCACTTCA-----GTAGGAGACAGGGTCAGC 555
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 556 ATCAGTCCAGAGGCC---AGTCAGGATGTATATATGCTGTGCTGGTATCAACAGAAA 612
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 613 CCAGGA-----CAATCTCTAAACTCTGATTACTCGGCATCTCTCCCGGTACACTGGA 666
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 667 GTC-----CCTTCTCGCTTCACTGGCAGTGGCTCGGCGCGGATTTCCTTTC 714

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Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSer----- 116
Db 715 ACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTCTGTGACCAACATTTTGGT 774
Qy 117 -----AlaLeuSerAsn 120
Db 775 ACTCCATTTCAGTTCGGCTCGGGACAAATAATTGGAGATCAAAAGCTCTAGAGATCAGCAAC 834
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 835 TCGGTGATGTTACTTTCAGTTCGTGTCGCGCAGTCTCTTCAGAAAGTGAACCTCTACTACTACC 894
Qy 141 ---ProAlaProArgProProThrProAla---ProThrIleAlaSerGlnProLeuSer 158
Db 895 AAGCCAGTGTGCGAACTCCCTCAGCTGTGCACCTACCGGACATCTCAGCCCC----- 948
Qy 159 LeuArgProGluAlaCysArgProAlaAlaGlyGlyAlaGly 172
Db 949 CAGAGACCAGAGATTGTTCGCCCCCGTGGCTCAGTGAAGGGG 990

RESULT 14
US-08-751-359-21
; Sequence 21, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751.359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-751-359-21

Alignment Scores:
Pred. No.: 0.133 Length: 5526
Score: 136.00 Matches: 57
Percent Similarity: 38.1% Conservative: 31
Best Local Similarity: 24.7% Mismatches: 74
Query Match: 13.0% Indels: 69
DB: 3 Gaps: 11

US-10-804-763-3 (1-198) x US-08-751-359-21 (1-5526)

Qy 7 AlaLeuLeuLeuProLeuAla-----LeuLeuLeuHisAlaAla----- 19
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Db 604 GCCGTTTTTCCCTCTCTCTCTCTCCCTCTCCAGGTCCCTGGTGACGAGCGGTGACT 663
Qy 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
Db 664 CAGCGGTCTCTCGGTGTGAGCAACCGG-----GGAGAAACCGTC 702
Qy 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
Db 703 AAGATCACCCTGC-----TCCGGGATAGGAGCTACTATGGCTGG---TACCAG 747
Qy 60 ProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLys 79
Db 748 CAGAGGACCTGCGCAGTGGCCCTGTCTACTGTGATCTAAGTAAACACAGACAGACCTCG 807
Qy 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
Db 808 GACATC-----CCTTCAGGATTCTCCGGTTCCAAATCCGGCTCCACAGCCACA 855
Qy 100 LeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSer 119
Db 856 TTAACCATCACTGGGGTCCCAAGCCGACGAGGCTGTCTATTACTGTGGGAGTGCAGAC 915
Qy 120 AsnSer-Ile----- 122
Db 916 AGCAGCAGTACTGTCTGCACGGTGACACAAACAATGGGAAATGATACAAAACCTCCTG 975
Qy 123 -----MetTyrPheSerHisPheVal-----ProValph 132
Db 976 CCAGTGAAGGAGCAGCTGATGGTTTTTACTGTCTCTCTTACAAGTCCACCTCCATT 1035
Qy 132 eLeuPro-----AlaLysProThrThrThrProAlaProArg----- 144
Db 1036 CCTGCCTGTCTGCAGCGCCCGGTCTCTCTGTGGTTCCAGGCTGCACCCAGGTCCAG 1095
Qy 145 -----ProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgPr 161
Db 1096 CTGGCTGAATCCCTGCCATCCACATCCACATTGTAGTGTCCCC----- 1141
Qy 161 oGluAlaCysArgProAlaAlaGlyAlaGlyAsnArgArgValCysLysCysPr 181
Db 1142 -----TGCATGCACGAGGCTGGCAGCTCTCTCATCTCTGCTCTCCACTGAGACCAC 1194
Qy 181 oArgProValValLysSerGlyAspLysPro 191
Db 1195 CTGCCAGCCCATCTGTGGAGGGCCACCACCA 1225

RESULT 15
US-08-907-146-21
; Sequence 21, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907.146
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-907-146-21

Alignment Scores:
Pred. No.: 0.133 Length: 5526
Score: 136.00 Matches: 57
Percent Similarity: 38.1% Conservative: 31
Best Local Similarity: 24.7% Mismatches: 74
Query Match: 13.0% Indels: 69
DB: 3 Gaps: 11

US-10-804-763-3 (1-198) x US-08-907-146-21 (1-5526)

Qy 7 AlaLeuLeuLeuProLeuAla-----LeuLeuLeuHisAlaAla----- 19
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-907-146-21

Alignment Scores:
Pred. No.: 0.133 Length: 5526
Score: 136.00 Matches: 57
Percent Similarity: 38.1% Conservative: 31
Best Local Similarity: 24.7% Mismatches: 74
Query Match: 13.0% Indels: 69
DB: 3 Gaps: 11

US-10-804-763-3 (1-198) x US-08-907-146-21 (1-5526)

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Db      604 GCCGTTTCTCCCTCTCTCCCTCTCCCTCTCCAGGTTCCCTGGTCAGGCGCTGACT 663

QY      20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
Db      664 CAGCCGTCTCGGTCTCAGCAACCG-----GGAGAAACCGTC 702

QY      40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
Db      703 AAGATCACCTGC-----TCCGGGATAGGAGCTACTATGGCTGG---TACCAG 747

QY      60 ProArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLys 79
Db      748 CAGAGGCACCTGGCAGTGCCTCTCATCTGTATCTATGCTAACCAACAGACCCCTCG 807

QY      80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
Db      808 GACATC-----CCTTCAGATTCTCCGGTTCAAATCCGGTCCACGCCACA 855

QY      100 LeuThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSer 119
Db      856 TTAACCATCACTGGGTCAGCCGACGACGAGGCTGTCTATTACTGTGGGAGTGCAGAC 915

QY      120 AsnSer-Ile----- 122
Db      916 AGCAGCATGCTGTCGACGTCACAAAGCAATGGGGAATGATACAAAACCTCCTG 975

QY      123 -----MetTyrPheSerHisPheVal-----ProValPhe 132
Db      976 CCAGTGCAGGAGCAGCTGATGGTTTTTACTGTCTCTCTTACAAGTCCACCTCCATT 1035

QY      132 eLeuPro-----AlaLysProThrThrProAlaProArg----- 144
Db      1036 CCGTCCCTGTGTGTCAGCGCCCGGGTCTCTCGTGGCTCCAGGCTGCACCCAGGTCCAG 1095

QY      145 -----ProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgPr 161
Db      1096 CTGGCTGAATCCCTGCCATCCAAACATCCACCATTTGTAGTGTCCC----- 1141

QY      161 oGluAlaCysArgProAlaAlaGlyAlaGlyAlaGlyAsnArgArgValCysLysCysPr 181
Db      1142 -----TGCATGACACCGGCTGGCAGCTCTCATCTGCTCTGCCACTGAGACCAC 1194
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QY 181 oArgProValValLysSerGlyAspLysPro 191
Db 1195 CTGCCCAGCCCATGCTGGAGGCCACCACCA 1225

Search completed: May 29, 2006, 12:46:48
Job time : 220.633 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:14:31 ; Search time 1111.18 Seconds
(without alignments)
3284.288 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA Main -QPWT=fastap -SUFFIX=rnpsbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=spect -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss804
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-NO WMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Published Applications NA Main:

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
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| Sequence 4, Appli | | | | | |

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| 2 | 1043 | 100.0 | 2150 | 10 | US-10-804-763-4 |
| 3 | 1006.5 | 96.5 | 708 | 9 | US-10-804-762-28 |
| 4 | 1006.5 | 96.5 | 708 | 10 | US-10-804-763-28 |
| 5 | 1006.5 | 96.5 | 1060 | 6 | US-10-207-655-173 |
| 6 | 1006.5 | 96.5 | 1060 | 8 | US-10-641-643-1014 |
| 7 | 1006.5 | 96.5 | 2261 | 9 | US-10-804-762-2 |
| 8 | 1006.5 | 96.5 | 2261 | 10 | US-10-888-313A-99 |
| 9 | 1006.5 | 96.5 | 2261 | 10 | US-10-804-763-2 |
| 10 | 926.5 | 88.8 | 692 | 7 | US-10-378-393-2 |
| 11 | 926.5 | 88.8 | 1995 | 7 | US-10-378-393-6 |
| 12 | 926 | 88.8 | 2411 | 7 | US-10-378-393-10 |
| 13 | 921.5 | 88.4 | 689 | 7 | US-10-378-393-19 |
| 14 | 921.5 | 88.4 | 690 | 7 | US-10-378-393-12 |
| 15 | 921.5 | 88.4 | 1987 | 7 | US-10-378-393-17 |
| 16 | 921.5 | 88.4 | 8858 | 7 | US-10-378-393-1 |
| 17 | 909 | 87.2 | 2134 | 9 | US-10-723-860-5746 |
| 18 | 869.5 | 83.4 | 708 | 9 | US-10-804-762-26 |
| 19 | 869.5 | 83.4 | 708 | 10 | US-10-804-763-26 |
| 20 | 804 | 77.1 | 597 | 9 | US-10-804-763-6 |
| 21 | 804 | 77.1 | 597 | 10 | US-10-804-763-6 |
| 22 | 620.5 | 59.5 | 785 | 9 | US-10-804-763-22 |
| 23 | 620.5 | 59.5 | 785 | 10 | US-10-804-763-22 |
| 24 | 546 | 52.3 | 2179 | 9 | US-10-804-762-20 |
| 25 | 546 | 52.3 | 2179 | 10 | US-10-804-763-20 |
| 26 | 532 | 51.0 | 2001 | 9 | US-10-804-763-18 |
| 27 | 532 | 51.0 | 2001 | 10 | US-10-804-763-18 |
| 28 | 510.5 | 48.9 | 1330 | 9 | US-10-804-763-16 |
| 29 | 510.5 | 48.9 | 1330 | 10 | US-10-804-763-16 |
| 30 | 471.5 | 45.2 | 922 | 7 | US-10-311-455-2246 |
| 31 | 471.5 | 45.2 | 922 | 7 | US-10-240-485-186 |
| 32 | 439.5 | 42.1 | 1229 | 9 | US-10-804-763-24 |
| 33 | 439.5 | 42.1 | 1229 | 10 | US-10-804-763-24 |
| 34 | 401 | 38.4 | 922 | 7 | US-10-311-455-2245 |
| 35 | 401 | 38.4 | 922 | 7 | US-10-240-485-185 |
| 36 | 380 | 36.4 | 1010 | 9 | US-10-804-762-14 |
| 37 | 380 | 36.4 | 1010 | 10 | US-10-804-763-14 |
| 38 | 380 | 36.4 | 1010 | 16 | US-11-136-527-2941 |
| 39 | 352.5 | 33.8 | 743 | 3 | US-09-477-737-2 |
| 40 | 350.5 | 33.6 | 804 | 9 | US-10-804-762-12 |
| 41 | 350.5 | 33.6 | 744 | 10 | US-10-804-763-12 |
| 42 | 349.5 | 33.5 | 1452 | 9 | US-10-804-762-10 |
| 43 | 349.5 | 33.5 | 1452 | 10 | US-10-804-763-10 |
| 44 | 320.5 | 30.7 | 933 | 9 | US-10-804-762-8 |
| 45 | 320.5 | 30.7 | 933 | 9 | US-10-804-762-30 |

ALIGNMENTS

RESULT 1
US-10-804-762-4
; Sequence 4, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allorejection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-4

Alignment Scores: 6.78e-99 Length: 2150
Pred. No.: 1043.00 Matches: 198
Score:

imbar
long
seq

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Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x US-10-804-762-4 (1-2150)

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Db 120 ATGGCCCTTACCAGTGACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTGCCAACCCGACCTCGGCTGCTGCTCTTCCAGCGG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCGCTCCACCTTCTCTATACCTCTCCCAAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGGCTGGACACCCAGCGGTTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 479
Qy 121 SerLeuMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCGAAGCCACCACGAGG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGCAGACCCCTGTCTCGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGGGGTGCCGCGCAGCGCGGGGGCGCGAGGACCGAGACGTGTTTGCAATGT 659
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 198
Db 660 CCCCAGCGCTGTGGTCAATCGGAGACAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 2
US-10-804-763-4
; Sequence 4, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-4

Alignment Scores:
Pred. No.: 6,78e-99 Length: 2150
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservatives: 0

US-10-804-763-3 (1-198) x US-10-804-763-4 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
Db 120 ATGGCCCTTACCAGTGACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTTCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTGCCAACCCGACCTCGGCTGCTGCTCTTCCAGCGG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCGCTCCACCTTCTCTATACCTCTCCCAAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGGCTGGACACCCAGCGGTTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 479
Qy 121 SerLeuMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCGAAGCCACCACGAGG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGCAGACCCCTGTCTCGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGGGGTGCCGCGCAGCGCGGGGGCGCGAGGACCGAGACGTGTTTGCAATGT 659
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 198
Db 660 CCCCAGCGCTGTGGTCAATCGGAGACAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 3
US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransplantation
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Alignment Scores:
Pred. No.: 1.17e-95 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
```

```
Query Match: 96.5% Indels: 37
DB: 9 Gaps: 1

US-10-804-763-3 (1-198) x US-10-804-762-28 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 1 ATGGGCTTACCAAGTACCGCCCTTGCTCCGCGCTGGCTTGTCTGCCACGCCGCGCAG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 61 CCGAGCCAGTTCGGGGTGTGGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 121 CTGAAGTGCAGGTGCTGCTCCAAACCGACGCTGGGCTGCTGGTGGCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 181 CGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTCCT 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 361 TCCATCATGTACTTCAGCCACTTCGTCGGGCTTCTTCTGCGGAGGAGGAGGAGGAG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 421 CCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 481 CCAGAGGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 171 ----- 171
DB 541 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 600
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 601 GTTATCACCTTTACTGCAACACACAGGAAACCGAGACGTTGTTGCAAAATGTCCTCCGCGCT 660

RESULT 4
US-10-804-763-28
; Sequence 28, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-804-763-3 (1-198) x US-10-804-763-28 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 1 ATGGGCTTACCAAGTACCGCCCTTGCTCCGCGCTGGCTTGTCTGCCACGCCGCGCAG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 61 CCGAGCCAGTTCGGGGTGTGGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 121 CTGAAGTGCAGGTGCTGCTCCAAACCGACGCTGGGCTGCTGGTGGCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 181 CGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTCCT 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTGGCCCTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 361 TCCATCATGTACTTCAGCCACTTCGTCGGGCTTCTTCTGCGGAGGAGGAGGAGGAG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 421 CCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 481 CCAGAGGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
QY 171 ----- 171
DB 541 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 600
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 601 GTTATCACCTTTACTGCAACACACAGGAAACCGAGACGTTGTTGCAAAATGTCCTCCGCGCT 660

RESULT 5
US-10-207-655-173
; Sequence 173, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 173
; LENGTH: 1060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-173

Alignment Scores:
Pred. No.: 1.94e-95 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 6 Gaps: 1

US-10-804-763-3 (1-198) x US-10-207-655-173 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCGAG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGACCTGGGAGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGGGCTCTTCCAGCGC 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGGCGCGCGCCAGTCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTGTCTCTC 365

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGACGCACTTCCGCGCAGAGAACGAGGGCTACTATTCTGCTCGGCGCTTGAGCAAC 425

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTCAGGCACCTTCGTCGGGTCTTCTGCCAGCAAGCCCAAGCAGC 485

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACCAACACCGCGCCACCATCGGTCGCGACGCCCTGTCTCTGCGC 545

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 546 CCAGAGCGGTGCGCGCCAGCGCGCGGCGCGCAGTGTCACAGAGGGGCTGGAATTGCGC 605

Qy 171 ----- 171
Db 606 TGTGATATCTACATCTGGGGCGCCCTTGGCGGAGACTTGTGGGTCTTCTCTGTCACTG 665

Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGTTGTTGCAAAATGTCCCGGCT 725

Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 726 GTGGTCAATCGGGAGACAAGCCAGCCTTTCGGCGAGATACGTC 770

RESULT 6
US-10-641-643-1014
; Sequence 1014, Application US/10641643
; Publication No. US2004007003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
```

```
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179145
; SEQUENCE DESCRIPTION: SEQ ID NO: 1014 :
US-10-641-643-1014
```

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Alignment Scores:
Pred. No.: 1.94e-95 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 8 Gaps: 1

US-10-804-763-3 (1-198) x US-10-641-643-1014 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 66 ATGGCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCGAG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGACCTGGGAGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGGGCTCTTCCAGCGC 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGGCGCGCGCCAGTCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTGTCTCTC 365

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGACGCACTTCCGCGCAGAGAACGAGGGCTACTATTCTGCTCGGCGCTTGAGCAAC 425
```

```
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCGAAGCCACACGAGC 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGAGCCACCAACACCGCGGCCACCATCGCGTCGAGCCCTGTCCCTGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 546 CCAGAGCGGTGCGGCCACGCGCGGGGGCGGAGTGCACACAGAGGGGTGGACTTCGCC 605
QY 171 ----- 171
Db 606 TGTGATATCTACATCTGGCGCGCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCTAC 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCCCTTTACTGCAACCCACAGGAACCGAAGACGTGTTTGCAAAATGTCCCG 725
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 726 GTGGTCAATCGGGAGACAGCCAGCCCTTTTCGGCGAGATACGTC 770
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RESULT 7

US-10-804-762-2

; Sequence 2, Application US/10804762

; Publication No. US20050042217A1

; GENERAL INFORMATION:

; APPLICANT: QI, Yan

; APPLICANT: Zhang, Xianghua

; APPLICANT: Konigsberg, Paula

; TITLE OF INVENTION: Specific Inhibition of Allotransplantation

; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)

; CURRENT APPLICATION NUMBER: US/10/804,762

; PRIOR FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: US 60/456,378

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 2261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-804-762-2

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 4,94e-95 | Length: | 2261 |
| Score: | 1006.50 | Matches: | 197 |
| Percent Similarity: | 83.8% | Conservative: | 0 |
| Best Local Similarity: | 83.8% | Mismatches: | 1 |
| Query Match: | 96.5% | Indels: | 37 |
| DB: | 9 | Gaps: | 1 |

US-10-804-763-3 (1-198) x US-10-804-762-2 (1-2261)

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QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCTTTACCAAGTACCGCCCTTGTCTCGCGCTGGCGCTTGTCTCCAGCCGCCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTCTGTGTCTCAACCCGACGTCGGGCTGTCTGTGGTCTTCTCCAGCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGAGTCCACCTTCTCTCTATACCTCTCTCCAAAAAAGCCCAAGCG 359
```

```
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGCACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTCCTC 419
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTTGAGCGACTTCGCCGAGAGAACGAGGGCTACTATTCTGTCTCGCCCTTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGGAGCCACACGAGC 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGAGCCACCAACACCGCGGCCACCATCGCGTCGAGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 600 CCAGAGCGGTGCGGCCACGCGCGGGGGCGGAGTGCACACAGAGGGGTGGACTTCGCC 659
QY 171 ----- 171
Db 660 TGTGATATCTACATCTGGCGCGCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCTAC 719
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATCACCCCTTTACTGCAACCCACAGGAACCGAAGACGTGTTTGCAAAATGTCCCG 779
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAATCGGGAGACAGCCAGCCCTTTTCGGCGAGATACGTC 824
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RESULT 8

US-10-888-313A-99

; Sequence 99, Application US/10888313A

; Publication No. US20050100934A1

; GENERAL INFORMATION:

; APPLICANT: AXEL, Kevin

; APPLICANT: LEE, Kevin

; APPLICANT: STRAPPS, Walter

; APPLICANT: BARNEA, Gilad

; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction

; FILE REFERENCE: SENTI 203.2

; CURRENT APPLICATION NUMBER: US/10/888,313A

; CURRENT FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: 60/566,113

; PRIOR FILING DATE: 2004-04-27

; PRIOR APPLICATION NUMBER: 60/511,918

; PRIOR FILING DATE: 2003-10-15

; PRIOR APPLICATION NUMBER: 60/485,968

; PRIOR FILING DATE: 2003-07-09

; NUMBER OF SEQ ID NOS: 101

; SEQ ID NO 99

; LENGTH: 2261

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-888-313A-99

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 4,94e-95 | Length: | 2261 |
| Score: | 1006.50 | Matches: | 197 |
| Percent Similarity: | 83.8% | Conservative: | 0 |
| Best Local Similarity: | 83.8% | Mismatches: | 1 |
| Query Match: | 96.5% | Indels: | 37 |
| DB: | 10 | Gaps: | 1 |

US-10-804-763-3 (1-198) x US-10-888-313A-99 (1-2261)

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QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCTTTACCAAGTACCGCCCTTGTCTCGCGCTGGCGCTTGTCTCCAGCCGCCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
```

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Db 180 CCGAGCCAGTTCCTGGGCTGCGCGCTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCTGTCCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGGACCGCGCCACCATCGCTCGCAGCGAAGCCACCAGCAG 539
Qy 141 ProGluAlaCysArgProAlaAlaGlyGlyAla 171
Db 600 CCAGAGGCGTGCCTGGCGCACGCGCGGGGGCGCAGTGCACAGGGGGCTGGACTTCGCC 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCACTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATACCCCTTTACTGCACACACAGGAACCGAAGACGTGTTTGCAAAATGCCCCGGCCT 779

184 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
780 GTGGTCAATCGGAGACAGCCAGCCTTTCGGCGAGATACGTC 824
```

RESULT 9

```
US-10-804-763-2
; Sequence 2, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-2
```

```
Alignment Scores:
Pred. No.: 4,948-95 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 10 Gaps: 1
```

```
US-10-804-763-3 (1-198) x US-10-804-763-2 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 120 ATGGCCCTTACAGTGAGCGGCTTCTCTCGCGCTGGCTTGTCTGTCTCCAGCCCGCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTTCGGGGTGTGCGCCCTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCTGTCCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGGACGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTTCAGCCACTTCGTGCGGCTTCTCTGCGGCAAGAGCCACCAGCAG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGAGGCGTGCCTGGCGCACGCGCGGGGGCGCAGTGCACAGGGGGCTGGACTTCGCC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla 171
Db 600 CCAGAGGCGTGCCTGGCGCACGCGCGGGGGCGCAGTGCACAGGGGGCTGGACTTCGCC 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCACTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATACCCCTTTACTGCACACACAGGAACCGAAGACGTGTTTGCAAAATGCCCCGGCCT 779

184 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
780 GTGGTCAATCGGAGACAGCCAGCCTTTCGGCGAGATACGTC 824

RESULT 10
US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-378-393-2

Alignment Scores:

Pred. No.: 2,91e-87 Length: 692
Score: 926.50 Matches: 181
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.8% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-2 (1-692)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 36 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCGAG 95
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 96 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACTTGGAACTTGGCGGAGACAGTGGAG 155
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 156 CTGAAGTGCAGGTGCTGTCTCAACCGACGTGGGCTGTCTGGCTCTTCCAGCGG 215
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 216 CCGCGCGCGCGCCAGTCCCACTTCTCTATACCTTCCCAAAACCAAGCCCAAGCGG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 276 GCCGAGGGGCTGGACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 335
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 336 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 395
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 396 TCCATCATGTACTTCAGCGCACTTCGTGCGGTCTTCTGCCAGCGAAAGCCACCGAGC 455
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 456 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGACGCGGGGTGCACTTCGCC 515
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 516 CCAGAGGGGTGCGGCCACCGCGCGGGGGCGGCGAGTGCACACGAGGGGTGCACTTCGCC 575
QY 171 ----- 171
DB 576 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCACGTG 635
QY 172 -----GlyAsnArgArgArgValCysLysCysProArg 182
DB 636 GTTATCACCTTTACTGCAACACCAAGAACCGAAGACGTGTTTGCAAAATGTCGCCGG 692

RESULT 11

US-10-378-393-6

; Sequence 6, Application US/10378393

; Publication No. US20030182668A1

; GENERAL INFORMATION:

; APPLICANT: Bol, David K.

; APPLICANT: Carboni, Joan M.

; APPLICANT: Rowley, Ronald B.

; APPLICANT: Wong, Tai W.

; APPLICANT: Lee, Francis Y.

; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED

; FILE REFERENCE: D0254 NP

; CURRENT APPLICATION NUMBER: US/10/378,393

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/360,889

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 1995

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-378-393-6

Alignment Scores:

Pred. No.: 1.08e-86 Length: 1995
Score: 926.50 Matches: 181
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.8% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-6 (1-1995)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 53 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCGAG 112
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 113 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACTTGGAACTTGGCGGAGACAGTGGAG 172
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 173 CTGAAGTGCAGGTGCTGTCTCAACCGGACTTGGGCTGTCTGGGTCTTTCAGCGG 232
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 233 CCGCGCGCGCGCCAGTCCCACTTCTCTCTATACCTTCTCCAAACCAAGCCCAAGCGG 292
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 293 GCCGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 352
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 353 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTGGGCCCTGAGCAAC 412
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 413 TCCATCATGTACTTCAGCGCACTTCGTGCGGTCTTCTGCCAGCGAAGCCACCGAGC 472
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 473 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGACGCGCCCTGTCTCTGCGC 532
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 533 CCAGAGGGGTGCGGCCACCGCGGGGGCGGCGAGTGCACACGAGGGGGTGGACTTCGCC 592
QY 171 ----- 171
DB 593 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCACGTG 652
QY 172 -----GlyAsnArgArgArgValCysLysCysProArg 182
DB 653 GTTATCACCTTTACTGCAACACCAAGAACCGAAGACGTGTTTGCAAAATGTCGCCGG 709

RESULT 12

US-10-378-393-10

; Sequence 10, Application US/10378393

; Publication No. US20030182668A1

; GENERAL INFORMATION:

; APPLICANT: Bol, David K.

; APPLICANT: Carboni, Joan M.

; APPLICANT: Rowley, Ronald B.

; APPLICANT: Wong, Tai W.

; APPLICANT: Lee, Francis Y.

; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED

; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.: 1,54e-86 Length: 2411
Score: 926.00 Matches: 184
Percent Similarity: 76.2% Conservatives: 2
Best Local Similarity: 75.4% Mismatches: 6
Query Match: 88.8% Indels: 52
DB: 7 Gaps: 2

US-10-804-763-3 (1-198) x US-10-378-393-10 (1-2411)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 36 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCCTTGCTCTCCACGCCGCCAGG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCCGGGTGTCCCGCTGGATCGACCTGGAACTGGGGGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTCGGCTGCTGTCTCTCCAGCG 215
Qy 61 ArgGlyAlaAlaLaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCTGCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCGCTGAGCAAC 395
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCGGAGAGTGGGGCTTCCGCG 455
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACCAACACCGCGGCCACCATCGCTGCGACGCCCTGTGCTGCGC 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 516 CCAGAGGCGTGCCGCGACCGCGGGGCGGAGTGACACAGAGGGGCTGGACTTCGCC 575
Qy 171 ----- 171
Db 576 TGTGATATCTACATCTGGCGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTGTGCACTG 635
Qy 172 -----GlyAsnArgArgArgValCysLysCysPro----- 181
Db 636 GTTATCACCTTTACTGCAACACACAGGAAACCGAGACGTGTTGCAATGTCCTCCGAG 695
Qy 182 -----ArgProValValLysSerGly 188
Db 696 TCTACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCCTGACACCTAGCGGA 755
Qy 189 AspLysProSer 192

Db 756 GCGATGCCCAAC 767
RESULT 13
US-10-378-393-19
; Sequence 19 Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-19

Alignment Scores:
Pred. No.: 9,72e-87 Length: 689
Score: 921.50 Matches: 180
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.4% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-19 (1-689)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 36 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCCTTGCTCTCCACGCCGCCAGG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCCGGGTGTCCCGCTGGATCGACCTGGAACTGGGGGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTCGGCTGCTGTCTCTCTCCAGCG 215
Qy 61 ArgGlyAlaAlaLaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTGGGGGACACCTTCTGCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCGCTGAGCAAC 395
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCGGAGAGTGGGGCTTCCGCG 455
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACCAACACCGCGGCCACCATCGCTGCGACGCCCTGTGCTGCGC 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 516 CCAGAGGCGTGCCGCGACCGCGGGGCGGAGTGACACAGAGGGGCTGGACTTCGCC 575

QY 171 ----- 171

Db 576 TGTGATATCTACATCTGGGGCCCTTGGCGGGACTTGTGGGTCTCTCTGTGTCACGTG 635

QY 172 -----GlyAsnArgArgArgValCysLysCysPro 181

Db 636 GTTATCACCCCTTACTGCAACACAGGAAACCGAAGACGTGTTTGCAAAATGTCCC 689

RESULT 14

US-10-378-393-12

; Sequence 12, Application US/10378393

; Publication No. US20030182668A1

; GENERAL INFORMATION:

; APPLICANT: Bol, David K.

; APPLICANT: Carboni, Joan M.

; APPLICANT: Rowley, Ronald B.

; APPLICANT: Wong, Tai W.

; APPLICANT: Lee, Francis Y.

; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED

; FILE REFERENCE: D0254 NP

; CURRENT APPLICATION NUMBER: US/10/378,393

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/360,889

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 12

; LENGTH: 690

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-378-393-12

Alignment Scores:

Pred. No.: 9,738-87 Length: 690

Score: 921.50 Matches: 180

Percent Similarity: 82.6% Conservative: 0

Best Local Similarity: 82.6% Mismatches: 1

Query Match: 88.4% Indels: 37

DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-12 (1-690)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 36 ATGGCCTTACCAAGTACCGCCCTTGCTCTCGCGCTGGCCTTGCTGCTCCACGCCCGCAGG 95

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 96 CCGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 155

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 156 CTGAAGTGCAGGTGCTGTGTCACACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGG 215

QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

Db 216 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAAACAAGCCCAAGCGG 275

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 276 GCGGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 335

QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 395

QY 121 SerIleMetTyrPheSerHisPheValProValPheProAlaLysProThrThrThr 140

Db 396 TCCATCATGTACTTCAGGCACCTTCGTGGCGGTCTCTCGCCAGCAAGCCCAACACAGAGG 455

QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 456 CCAGCGCGCGACCAACACCGCGCCACCATCGCTCGCAGCCCTGTCCCTGGCG 515

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171

Db 516 CCAGAGGCGTGC CGCGCGCGCGCGCGAGTGCACACGAGGGGGTGGACTTCGCC 575

QY 171 ----- 171

Db 576 TGTGATATCTACATCTGGGGCCCTTGGCGGGACTTGTGGGTCTCTCTGTGTCACGTG 635

QY 172 -----GlyAsnArgArgArgValCysLysCysPro 181

Db 636 GTTATCACCCCTTACTGCAACACAGGAAACCGAAGACGTGTTTGCAAAATGTCCC 689

RESULT 15

US-10-378-393-17

; Sequence 17, Application US/10378393

; Publication No. US20030182668A1

; GENERAL INFORMATION:

; APPLICANT: Bol, David K.

; APPLICANT: Carboni, Joan M.

; APPLICANT: Rowley, Ronald B.

; APPLICANT: Wong, Tai W.

; APPLICANT: Lee, Francis Y.

; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED

; FILE REFERENCE: D0254 NP

; CURRENT APPLICATION NUMBER: US/10/378,393

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/360,889

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 17

; LENGTH: 1987

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-378-393-17

Alignment Scores:

Pred. No.: 3,618-86 Length: 1987

Score: 921.50 Matches: 180

Percent Similarity: 82.6% Conservative: 0

Best Local Similarity: 82.6% Mismatches: 1

Query Match: 88.4% Indels: 37

DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-17 (1-1987)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 37 ATGGCCTTACCAAGTACCGCCCTTGCTCTCGCGCTGGCCTTGCTGCTCCACGCCCGCAGG 96

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 97 CCGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 156

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 157 CTGAAGTGCAGGTGCTGTGTCACACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGG 216

QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

Db 217 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAAACAAGCCCAAGCGG 276

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 277 GCGGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 336

QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

Db 337 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 396

GenCore version 5.1.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:15:35 ; Search time 19.6628 Seconds
(without alignments)
1705.079 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/abss/ABSSWEB.spool/US10804763/runat_26052006.165105.14645/app_query.fasta_1
-DB=Published Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs06p
-USER=US10804763 @CGN 1 1 39 @runat_26052006.165105.14645 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New.*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|--------|-------------|------|-------------------|
| 1 | 1006.5 | 96.5 | 2261 | US-10-511-937-415 |
| 2 | 140.5 | 13.5 | 1912 | Sequence 415, App |
| 3 | 122 | 11.7 | 944 | Sequence 1818, Ap |
| 4 | 120 | 11.5 | 720 | Sequence 1585, Ap |
| 5 | 120 | 11.5 | 2081 | Sequence 39, Appl |
| 6 | 118 | 11.3 | 337 | Sequence 2348, Ap |
| 7 | 117 | 11.2 | 707 | Sequence 35, Appl |
| 8 | 115 | 11.0 | 720 | Sequence 19, Appl |
| 9 | 114 | 10.9 | 720 | Sequence 7, Appl |
| | | | | Sequence 15, Appl |

| | | | | | | |
|----|-------|------|------|---|--------------------|-------------------|
| 10 | 113 | 10.8 | 336 | 7 | US-11-211-917-3 | Sequence 3, Appl |
| 11 | 113 | 10.8 | 720 | 7 | US-11-211-917-55 | Sequence 55, Appl |
| 12 | 112 | 10.7 | 336 | 7 | US-11-211-917-11 | Sequence 11, Appl |
| 13 | 112 | 10.7 | 336 | 7 | US-11-211-917-93 | Sequence 93, Appl |
| 14 | 112 | 10.7 | 722 | 6 | US-10-503-433B-22 | Sequence 22, Appl |
| 15 | 112 | 10.7 | 796 | 6 | US-10-503-433B-24 | Sequence 24, Appl |
| 16 | 111.5 | 10.7 | 885 | 7 | US-11-154-103-33 | Sequence 33, Appl |
| 17 | 111 | 10.6 | 337 | 7 | US-11-211-917-51 | Sequence 51, Appl |
| 18 | 110.5 | 10.6 | 792 | 6 | US-10-503-433B-21 | Sequence 21, Appl |
| 19 | 110 | 10.5 | 337 | 7 | US-11-239-308-15 | Sequence 15, Appl |
| 20 | 110 | 10.5 | 704 | 6 | US-10-503-433B-15 | Sequence 15, Appl |
| 21 | 110 | 10.5 | 801 | 6 | US-10-503-433B-14 | Sequence 14, Appl |
| 22 | 109 | 10.5 | 764 | 6 | US-10-503-433B-11 | Sequence 11, Appl |
| 23 | 108 | 10.4 | 720 | 7 | US-11-211-917-31 | Sequence 31, Appl |
| 24 | 108 | 10.4 | 720 | 7 | US-11-211-917-63 | Sequence 63, Appl |
| 25 | 108 | 10.4 | 720 | 7 | US-11-211-917-79 | Sequence 79, Appl |
| 26 | 108 | 10.4 | 720 | 7 | US-11-211-917-101 | Sequence 101, App |
| 27 | 108 | 10.4 | 1954 | 7 | US-11-293-697-1648 | Sequence 1648, Ap |
| 28 | 107 | 10.3 | 735 | 6 | US-10-503-433B-12 | Sequence 12, Appl |
| 29 | 106 | 10.2 | 336 | 7 | US-11-211-917-27 | Sequence 27, Appl |
| 30 | 106 | 10.2 | 337 | 7 | US-11-211-917-59 | Sequence 59, Appl |
| 31 | 106 | 10.2 | 337 | 7 | US-11-211-917-75 | Sequence 75, Appl |
| 32 | 106 | 10.2 | 608 | 7 | US-11-301-554-908 | Sequence 908, App |
| 33 | 106 | 10.2 | 706 | 6 | US-10-503-433B-17 | Sequence 17, Appl |
| 34 | 106 | 10.2 | 4027 | 7 | US-11-169-140-1 | Sequence 1, Appl |
| 35 | 105.5 | 10.1 | 729 | 7 | US-11-154-103-20 | Sequence 20, Appl |
| 36 | 105 | 10.1 | 330 | 7 | US-11-254-679-59 | Sequence 59, Appl |
| 37 | 105 | 10.1 | 431 | 1 | US-09-784-950-71 | Sequence 71, Appl |
| 38 | 105 | 10.1 | 732 | 6 | US-10-503-433B-16 | Sequence 16, Appl |
| 39 | 104.5 | 10.0 | 2476 | 6 | US-10-196-749-585 | Sequence 585, App |
| 40 | 104 | 10.0 | 444 | 1 | US-09-784-950-63 | Sequence 63, Appl |
| 41 | 104 | 10.0 | 543 | 7 | US-11-301-554-970 | Sequence 970, App |
| 42 | 104 | 10.0 | 705 | 7 | US-11-211-917-23 | Sequence 23, Appl |
| 43 | 104 | 10.0 | 803 | 6 | US-10-503-433B-20 | Sequence 20, Appl |
| 44 | 103.5 | 9.9 | 5137 | 6 | US-10-505-928-802 | Sequence 802, App |
| 45 | 103 | 9.9 | 330 | 7 | US-11-254-679-43 | Sequence 43, Appl |

ALIGNMENTS

RESULT 1
US-10-511-937-415
; Sequence 415, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 415
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-415

Alignment Scores:

; LENGTH: 720

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Db 54 CTGCTATTCTCCTACCTCTCTACTCAGGGCACAGGGTCTCTGGGCCACTCTGCCCCGACT 113
Qy 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrVal 39
Db 114 CAGCGTGGCTCGGTCTCTGGTCTCTCT-----GGGCGAGTCGATC 152
Qy 40 GluLeuLysCysGlnValLeuLeuSerAsnPro-----ThrSerGly 53
Db 153 ACCGTCCTCTCTG-----ACTGGACCCAGCGGTGCGCTTTGGTCTCTGACTCT 200
Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaAspProThrPheLeuLeuTyrlLeu 73
Db 201 GTCTCTGGTATCAACACACCCAGGCAAGCC-----CCAGACTCATATTATGAT 254
Qy 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 255 GTCAGTCTCGGCCCTCGGGTGT-----TCTAGTCTGCTTCTCTGGCTCCAGG 302
Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrlTy 113
Db 303 TCCGGCAATACGGCTCTCCCTCACCATCTCTGGGCTCCAGGCTGAGGACGAGTCTACTTC 362
Qy 114 PheCysSerAla-----LeuSerAsnSerIleMetTyr----- 124
Db 363 TACTGCACTCATATACACACGTAAGTCTGTGATCTTTGGCGGAGGACCAAGGTGACC 422
Qy 125 -----PheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 423 GTCCTAGGTGAGTCTCTTCTCCCTCTCTCCCTCTCTCTCGACACAAATGCTCTACT 482
Qy 141 -----ProAlaProArgPro 145
Db 483 TTTCTGCTTTTCTCTGTCTGACTTCTCATCACCCCTTTTCCCTGCTGCTGCGGCC 542
Qy 146 -----ProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 543 TGAGCAGGACCTCTGCCCTTCTCTTCCGACCCGTGCACCTTTGCCCTTCATTACGT 602
Qy 161 -----ProGluAlaCysArg----- 165
Db 603 GGTTCATTTTGTGGCTTTTGGGAACAGGGCATCTGAGGGATGCTCTCTCTGGGAGACT 662
Qy 166 -----ProAlaAlaGlyClyAla-----GlyAsnArgArgValCysLys 179
Db 663 ATGGAGACACCCCTCGCCCTCGGGGCTGCTCTCGGGAATCGACACGTGTGACCAGA 720

RESULT 6
; Sequence 35, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIORITY FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-35
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Alignment Scores:
Pred. No.: 0.0697 Length: 337
Score: 118.00 Matches: 39
Percent Similarity: 46.4% Conservative: 12
Best Local Similarity: 35.5% Mismatches: 43
Query Match: 11.3% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-3 (1-198) x US-11-211-917-35 (1-337)
Qy 27 SerProLeuAspArgThrTrpAsnLeuGluGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTGCCGCTACCCCTGGAGCGCGCTCCATCTCTCTCGAGGTCAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGTGTCTGTATAGTAAATGATACAACTATTATTGGATTGGTACCTCGACAGAGCCAGG 138
Qy 63 AlaAlaAlaSerProThrPheLeuLeuTyrlLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCTCTGATCTATTTTGGTCTTAATCGG-----GCCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC-----CCTGACAGGTTCTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgArgGluAsnGluGlyTyrlTyrlPheCys--SerAlaLeuSerAsnSerI 122
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCATGCAAGTTTACAAACTCCA 300
Qy 122 leMetTyrPheSerHisPheValPro 130
Db 301 TT-----CACTTTCGGCCC 314

RESULT 7
US-10-503-433B-19
; Sequence 19, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 19
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-4
US-10-503-433B-19

Alignment Scores:
Pred. No.: 0.21 Length: 707
Score: 117.00 Matches: 29
Percent Similarity: 50.0% Conservative: 17
Best Local Similarity: 31.5% Mismatches: 38
Query Match: 11.2% Indels: 8
DB: 6 Gaps: 3

US-10-804-763-3 (1-198) x US-10-503-433B-19 (1-707)
Qy 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 439 GGGCAGAGGGTCACCATCTCTTGCACTGGGAGCAGCTCCACATCGGCGCAGGTATGAT 498
Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlLeu 73
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Db 499 GTACACTGGTATCAGCAGCTCCAGGAGCGGC-----CCCAAACTCCTCATCTATGCT 552
QY 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 553 AACACAAATCGGCCCTCAGGGTCTC-----CCTGACCGATCTCTGGCTCCAAG 600
QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyr 113
Db 601 TCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTAT 660
QY 114 PheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 661 TACTGTGGGCTCTTGATGACATGTAAAGTGGTAC 696

RESULT 8
US-11-211-917-7
; Sequence 7, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-7

Alignment Scores:
Pred. No.: 0.308 Length: 720
Score: 115.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 11.0% Indels: 10
DB: Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-7 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTGGGCTGCTAAATGCTCTGGATCCAGTGGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGCTGACTCTCCACTCTCCCTGCCCGTCACCCCTGGAGCGCGCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGCAGGTCTAGTCAGAGCCTCTGTATAGTAAATGGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCGAGG-----CAGTCTCCACAGCTCCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGCTC---CCTGACAGGTTTCAGTGGCAGTGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTC 339

RESULT 10
US-11-211-917-3
; Sequence 3, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
```

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Db 283 GATTTTACACTGAAATCAGCAGATTTGGAGGCTGAGGATGTTGGGTTTATTACTGTC 339

RESULT 9
US-11-211-917-15
; Sequence 15, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-15

Alignment Scores:
Pred. No.: 0.368 Length: 720
Score: 114.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 10.9% Indels: 10
DB: Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-15 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTGGGCTGCTAAATGCTCTGGATCCAGTGGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGCGCGCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGCAGGTCTAGTCAGAGCCTCTGTATAGTAAATGGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCGAGG-----CAGTCTCCACAGCTCCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGCTC---CCTGACAGGTTTCAGTGGCAGTGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTC 339

RESULT 10
US-11-211-917-3
; Sequence 3, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
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Align
Pred


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Db      79  CAGAGCCTCTGTTATAGTAATGATACAACTTTTGGATTGGTACCTGCAGAGCCAGG 138
Qy      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db      139  -----CAGTCTCCACAGCTCCTGATCTATTGGTCTTAATCGG-----GCCTCC 183
Qy      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      184  GGGGTC---CCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy      103  SerAspPheArgArgGluAsnGluGlyTyrTyrPheCys 115
Db      241  AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGC 279

```

RESULT 13

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US-11-211-917-93
; Sequence 93, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 93
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-93

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Alignment Scores:
Pred. No.:      0.205      Length:      336
Score:          112.00     Matches:      32
Percent Similarity: 45.2%   Conservative: 10
Best Local Similarity: 34.4% Mismatches:    41
Query Match:     10.7%     Indels:       10
DB:              7        Gaps:         4

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US-10-804-763-3 (1-198) x US-11-211-917-93 (1-336)
Qy      27  SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db      19  TCTCACCTCTCCCTCCCGCTACCCCTGAGAGCCGCGCTCCATCTCTGACAGGTCAGT 78
Qy      45  -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db      79  CAGAGCCTCTCTATAGTAATGATACAACTTTTGGATTGGTACCTGCAGAGCCAGG 138
Qy      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db      139  -----CAGTCTCCACAGCTCCTGATCTATTGGGTTCTTAATCGG-----GCCTCC 183
Qy      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      184  GGGGTC---CCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy      103  SerAspPheArgArgGluAsnGluGlyTyrTyrPheCys 115
Db      241  AGCAGAGTGGAGCTGAGGATGTTGGGGTTTATTACTGC 279

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RESULT 14

US-10-503-433B-22

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; Sequence 22, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 22
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-20
US-10-503-433B-22

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Alignment Scores:
Pred. No.:      0.53      Length:      722
Score:          112.00     Matches:      30
Percent Similarity: 48.3%   Conservative: 13
Best Local Similarity: 33.7% Mismatches:    38
Query Match:     10.7%     Indels:       8
DB:              6        Gaps:         3

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US-10-804-763-3 (1-198) x US-10-503-433B-22 (1-722)
Qy      36  GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db      438  GGGCAGAGGTCACCATCTCTTGCACTGGGACGAGCTCCAAATCGGGCAGGTACGAT 497
Qy      54  CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db      498  GTACACTGGTATCAGCAGCTCCAGGAACGGCC-----CCCAAACTCTCATCTATG 551
Qy      74  SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db      552  AACAAATCGGCCCTCAGGGGTC-----CCTGACCGATTTCTGGTCCCAAG 599
Qy      94  LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyr 113
Db      600  TCTGCACCTCAGCCTCCCTGCCCACATCAGTGGGCTCCGTCGAGATGAGGCTGATTAT 659
Qy      114  PheCysSerAlaLeuSerAsnSerIle 122
Db      660  TACTGTGCGCTTATGATGACAGTATT 686

```

RESULT 15

```

US-10-503-433B-24
; Sequence 24, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 24
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: F8 mutated clone 2-18
US-10-503-433B-24

Alignment Scores:
Pred. No.: 0.598 Length: 796
Score: 112.00 Matches: 29
Percent Similarity: 49.4% Conservative: 15
Best Local Similarity: 32.6% Mismatches: 37
Query Match: 10.7% Indels: 8
DB: 6 Gaps: 3

US-10-804-763-3 (1-198) x US-10-503-433B-24 (1-796)

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Qy 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 439 GGGCAGAGGGTCACCATCTCTTGCACTGGGAGCAGCTCCAACATCGGGCAGGTTTGGAT 498
Qy 54 CysSerTyrLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db 499 GTACACTGGTATCAGCAGCTCCCGAAGCGGCC-----CCCAACTCTCATCTATGGT 552
Qy 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 553 AACACAAATCGCCCTCAGGGGTC-----CCTGACCGATTCTCTGGCTCCAAG 600
Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyr 113
Db 601 TCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTAT 660
Qy 114 PheCysSerAlaLeuSerAsnSerIle 122
Db 661 TACTGTGGGCTCTCGATGACACTCTC 687
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Search completed: May 30, 2006, 04:18:02
Job time : 21.6628 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: May 30, 2006, 04:13:46 ; Search time 4304.33 Seconds
(without alignments)
3858.452 Million cell updates/sec

Title: US-10-804-763-3
Perfect score: 1043
Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/abs/ABSSWEB spool/US10804763/runat_26052006_165054_14448/app_query.fasta_1
-DB=EST_QPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes04
-USER=US10804763 @CN 1 1 7986 @runat_26052006_165054_14448 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -FGAPOP=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_hic: *
7: gb_est2: *
8: gb_est7: *
9: gb_est8: *
10: gb_est9: *
11: gb_gss1: *
12: gb_gss2: *
13: gb_gss3: *
14: gb_gss4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 1043 | 100.0 | 1948 | 6 | CR619549 full-length |
| 2 | 1030 | 98.8 | 755 | 9 | DR007174 TC101240 |
| 3 | 1008 | 96.6 | 705 | 2 | BI905877 603063005 |
| 4 | 981.5 | 94.1 | 789 | 2 | BI19839 603041366 |

| | | | | | | |
|----|-------|------|------|---|----------|--------------------|
| 5 | 966.5 | 92.7 | 804 | 2 | BI820808 | BI820808 603034019 |
| 6 | 963 | 92.3 | 549 | 9 | DB121562 | DB121562 DB121562 |
| 7 | 958 | 91.9 | 884 | 1 | AL552456 | AL552456 AL552456 |
| 8 | 952.5 | 91.3 | 838 | 9 | DA931234 | DA931234 DA931234 |
| 9 | 951.5 | 91.2 | 882 | 2 | BI820267 | BI820267 603036820 |
| 10 | 943.5 | 90.5 | 780 | 2 | BI760947 | BI760947 603043151 |
| 11 | 931 | 89.3 | 1109 | 4 | BX415859 | BX415859 BX415859 |
| 12 | 928 | 89.0 | 566 | 9 | DA943842 | DA943842 DA943842 |
| 13 | 900.5 | 86.3 | 949 | 8 | CO646993 | CO646993 ILLUMIGEN |
| 14 | 899 | 86.2 | 571 | 9 | DA952710 | DA952710 DA952710 |
| 15 | 899 | 86.2 | 576 | 9 | DA826683 | DA826683 DA826683 |
| 16 | 899 | 86.2 | 576 | 9 | DA956498 | DA956498 DA956498 |
| 17 | 899 | 86.2 | 578 | 9 | DA974329 | DA974329 DA974329 |
| 18 | 899 | 86.2 | 586 | 9 | DA942852 | DA942852 DA942852 |
| 19 | 899 | 86.2 | 594 | 2 | BI760884 | BI760884 603043751 |
| 20 | 899 | 86.2 | 602 | 9 | DB110509 | DB110509 DB110509 |
| 21 | 899 | 86.2 | 627 | 9 | DA371487 | DA371487 DA371487 |
| 22 | 899 | 86.2 | 840 | 2 | BI835165 | BI835165 603088746 |
| 23 | 897 | 86.0 | 600 | 9 | DB117237 | DB117237 DB117237 |
| 24 | 897 | 86.0 | 606 | 9 | DA936371 | DA936371 DA936371 |
| 25 | 897 | 86.0 | 611 | 9 | DB123733 | DB123733 DB123733 |
| 26 | 895.5 | 85.9 | 796 | 2 | BI911195 | BI911195 603062918 |
| 27 | 895 | 85.8 | 589 | 9 | DA941044 | DA941044 DA941044 |
| 28 | 895 | 85.8 | 620 | 9 | DA381496 | DA381496 DA381496 |
| 29 | 893 | 85.6 | 545 | 9 | DB102835 | DB102835 DB102835 |
| 30 | 893 | 85.6 | 571 | 9 | DB106910 | DB106910 DB106910 |
| 31 | 893 | 85.6 | 577 | 9 | DB200083 | DB200083 DB200083 |
| 32 | 893 | 85.6 | 599 | 9 | DA935416 | DA935416 DA935416 |
| 33 | 893 | 85.6 | 599 | 9 | DA938336 | DA938336 DA938336 |
| 34 | 892 | 85.5 | 704 | 9 | DN997301 | DN997301 TC111602 |
| 35 | 887 | 85.0 | 596 | 9 | DA940758 | DA940758 DA940758 |
| 36 | 887 | 85.0 | 597 | 9 | DA940156 | DA940156 DA940156 |
| 37 | 887 | 85.0 | 628 | 9 | DB123661 | DB123661 DB123661 |
| 38 | 882 | 84.6 | 580 | 9 | DA946587 | DA946587 DA946587 |
| 39 | 881 | 84.5 | 585 | 9 | DB110036 | DB110036 DB110036 |
| 40 | 881 | 84.5 | 592 | 9 | DA670538 | DA670538 DA670538 |
| 41 | 881 | 84.5 | 593 | 9 | DA421985 | DA421985 DA421985 |
| 42 | 881 | 84.5 | 593 | 9 | DB110805 | DB110805 DB110805 |
| 43 | 877 | 84.1 | 567 | 9 | DB118175 | DB118175 DB118175 |
| 44 | 874 | 83.8 | 569 | 9 | DB124972 | DB124972 DB124972 |
| 45 | 873 | 83.7 | 576 | 9 | DB121098 | DB121098 DB121098 |

ALIGNMENTS

CR619549 1948 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI070YG17 of Placenta Cot 25-normalized
of Homo sapiens (human).

ACCESSION CR619549.1 GI:50500356
VERSION HTG; CNSLT_cDNA.
KEYWORDS Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE

1. (bases 1 to 1948)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1948)

REFERENCE

Direct Submission
Genoscope.
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

JOURNAL

- Web : www.genoscope.cns.fr

REMARK

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source
1..1948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001070Y17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 2,33e-78 Length: 1948
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-3 (1-198) x CR619549 (1-1948)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 71 ATGGCTTACAGTACCGCCCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 130
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
DB 131 CCGAGCCAGTTCGGGGTGTCCGGCTGGATCGGACTGGACCTGGGCGGAGACAGTGGAG 190
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 191 CTGAAGTCCAGGTCTGTCTCCAAACCGACGTCGGGTGTCTGTCTCTCTTCCAGCGC 250
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 251 CGCGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCAAAACAAGCCCAAGCGC 310
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 311 GCCGAGGGGTGGACACCGCGGTCTCGGCGAGAGGTGGGGGACACCTTCTCTCTC 370
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 371 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGACCAAC 430
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 431 TCCATCATGTACTTCAGCCACTTCGTGCGGCTCTTCCTGCCAGCAAGCCACACGACG 490
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 491 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTGCGAGCCCTGTCTCTGCGC 550
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
DB 551 CCAGAGGGGTGCGCGGCG 610
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
DB 611 CCCCAGCCCTGTGGTCAAAATCGGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 664

RESULT 2

LOCUS DR007174 755 bp mRNA linear EST 17-MAY-2005
DEFINITION TC101240 Human spleen, large insert, pCMV expression library Homo sapiens cDNA clone TC101240 5' similar to Homo sapiens CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 2, mRNA sequence.
ACCESSION DR007174
VERSION DR007174.1 GI:66267047
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 755)
AUTHORS Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
TITLE High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
JOURNAL Unpublished (2005)
COMMENT Contact: Kovacs, KF
High throughput cDNA Cloning
Origene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: CDNA@origene.com
This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 Sp1 prime forward vector primer, Origene Technologies Inc.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC101240"
/tissue_type="Spleen"
/clone_lib="Human spleen, large insert, pCMV expression library"
/note="Organ: Spleen; Vector: pCMV6-XL4; Site 1: EcoRI; Site 2: XhoI/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

FEATURES

source
1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC101240"
/tissue_type="Spleen"
/clone_lib="Human spleen, large insert, pCMV expression library"
/note="Organ: Spleen; Vector: pCMV6-XL4; Site 1: EcoRI; Site 2: XhoI/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Alignment Scores:
Pred. No.: 8,76e-78 Length: 755
Score: 1030.00 Matches: 198
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 0
Query Match: 98.8% Indels: 1
DB: 9 Gaps: 0
US-10-804-763-3 (1-198) x DR007174 (1-755)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 37 ATGGCTTACAGTACCGCCCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 96
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 97 CCGAGCCAGTTCGGGGTGTCCGGCTGGATCGGACCTGGGCGGAGACAGTGGAG 156
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 157 CTGAAGTCCAGGTCTGTCTCCAAACCGACGTCGGGTGTCTGTCTCTTCCAGCGC 216
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 217 CG 276

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 277 GCGGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTCTC 336
QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrPheCysSerAlaLeuSerAen 120
Db 337 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGACCAAC 396
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 397 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTCTCCAGCAAGCCACACGAGC 456
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 457 CCAGCGCCGCGACCAACACCGCGCCACCATCGCTCGCAGCCCTGTCTCTCGCGC 516
QY 161 ProGluAlaCysArgProAlaLaGlyGlyAla-GlyAenArgAtgArgValCysLysCY 180
Db 517 CCAGAGGCGTGGCGGACGCGCGGGGGCGCTAGAGAAACCGAAGACGGTTTGCAAATG 576
QY 180 sProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 577 TCCCGCGCTGTGGTCAATCGGAGACAGCCAGCCCTTCGGCGAGATACGTC 631

RESULT 3

BI905877 705 bp mRNA linear EST 16-OCT-2001
LOCUS 603063005F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212128 5',
DEFINITION mRNA sequence.

ACCESSION BI905877

VERSION BI905877.1

KEYWORDS GI:16168472

SOURCE EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

1 (bases 1 to 705)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11532 row: j column: 01

High quality sequence stop: 705.

Location/Qualifiers

1..705

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5212128"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_lib="NIH MGC_118"

/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 6.08e-76 Length: 705
Score: 1008.00 Matches: 196
Percent Similarity: 99.0% Conservative: 0
Best Local Similarity: 99.0% Mismatches: 2
Query Match: 96.6% Indels: 1
DB: 2 Gaps: 0

US-10-804-763-3 (1-198) x BI905877 (1-705)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 65 ATGGCCTTACCAAGTGACCGCTTGTCTCGCGCTGGCCTTGTCTCCACGGCCGAGG 124
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 125 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 184
QY 41 LeuLysCysGlnValLeuLeuSerAenProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 185 CTGAAGTGCAGGTGCTGTCCAAACCGAGCTCGGGCTGTCTCGTGGCTCTTCCAGCCG 244
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 245 CCGCGCGCGCGCGCGAGTCCACCTTCCTTATACCTCTCCCAAAACAGCCCAAGCGG 304
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 305 GCGGAGGGGCTGGACACCGCGTTCGCGGCAAGAGGTTGGGGGACACCTTCGTCTC 364
QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrTyrPheCysSerAlaLeuSerAen 120
Db 365 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGC-CTGAGCAAC 423
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 424 TCCATCATGTACTTCAGCCACTTCGTGCGCGTTCCTCGCAGCAAGCCACACGAGC 483
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 484 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGGTCCGACCCCTGTCTCCCTGCGC 543
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAenArgArgValCysLysCys 180
Db 544 CCAGAGGCGTTCGCGCGCAGCGCGGGGGCGGAGGAAACCGAAGACGCTGTTTGCAAATGT 603
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 604 CCCCAGCGCTGTGTCAAAATCGGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 657

RESULT 4

BI819839

LOCUS

DEFINITION 603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5',

mRNA sequence.

ACCESSION BI819839

VERSION BI819839.1

KEYWORDS GI:15931389

SOURCE EST.

ORGANISM Homo sapiens

Homo sapiens

1 (bases 1 to 789)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

BI819839 789 bp mRNA linear EST 04-OCT-2001
LOCUS 603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5',
DEFINITION mRNA sequence.

ACCESSION BI819839

VERSION BI819839.1

KEYWORDS GI:15931389

SOURCE EST.

ORGANISM Homo sapiens

Homo sapiens

1 (bases 1 to 789)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM11454 row: d column: 18
 High quality sequence stop: 788.

FEATURES

source

1. 789
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5182049"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 Kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.3e-73 Length: 789
 Score: 981.50 Matches: 196
 Percent Similarity: 83.1% Conservative: 0
 Best Local Similarity: 83.1% Mismatches: 2
 Query Match: 94.1% Indels: 38
 DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI819839 (1-789)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
 Db 76 ATGGGCTTTACAGTGAACGCTTGTCTCGCGCTGGCTTGTCTCTCAAGCCGCGAG 135
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 136 CCGAGCCAGTTCCGGGTGTGCGCGTGTGATCGGACCTGGACCTGGCGGAGACAGTGGAG 195
 Qy 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 196 CTGAAGTCCCAAGTCTGTGTCACACCGACGTCGGGCTGTCTGTCTCTTCCAGCG 255
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 256 CGCGGCGCGCGCGCGAGTCCACCTTCTCTTATACCTCTCCAAACCAAGCCCAAGCGG 315
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 316 GCGGAGGGGTGGACACCGCGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCTCTC 375
 Qy 101 ThrLeuSerAppPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 376 ACCCTTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGCGCTGAGCAAC 435
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 436 TCCATCATGTACTTCAGGCACCTTCGTGCGGTCTTCCTGCGAGCGAAGCCACACGAGG 495
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 496 CCAGCGCGCGGACCAACACCGCGCCACCATCGGTCGCGAGCCCTGTCTCTCTGCGC 555
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 556 CCAGAGCGGTGCGCGGACGCGCGGGGCGCAGTGCACAGAGGGGGCTGGACTTCGCG 615
 Qy 171 ----- 171
 Db 616 CTGTGATATCTACATCTGGGCGCCCTTGGCGGGAGTTGTGGGTCCTTCTCTCTCACT 675

Qy 172 -----GlyAsnArgArgValCysLysCysProArgPr 183
 Db 676 GGTATTACCTTACTGCAACACAGGAGACGTCGTTCGCAATGTCCCGGCC 735
 Qy 183 oValValIysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 736 TGTGTCAAATCGGAGACAGCCAGCCTTTTCGGCGAGATACGTC 781

RESULT 5

BI820808 804 bp mRNA linear EST 04-OCT-2001
 LOCUS 603034019F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
 DEFINITION mRNA sequence.

ACCESSION BI820808

VERSION BI820808.1 GI:15932358

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 804)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11436 Row: e column: 06

High quality sequence stop: 802.

FEATURES

Location/Qualifiers

source

1. 804

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5175149"

/lab_host="DH10B"

/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector:

pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library is

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8 kb,

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed by C.

Gruber (Invitrogen). Research Genetics tracking code

ORIGIN

021. Note: this is a NIH_MGC Library."

Alignment Scores:

Pred. No.: 2.55e-72 Length: 804

Score: 966.50 Matches: 190

Percent Similarity: 81.5% Conservative: 0

Best Local Similarity: 81.5% Mismatches: 6

Query Match: 92.7% Indels: 37

DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI820808 (1-804)

Qy 3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuHisAlaAlaArgProSer 22
 Db 7 TTACAGTGACCGCTTCTCTCGCTGGCTTGTCTTCCACGCGCGAGCGGAGC 66
 Qy 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42

Db 67 CAGTCCCGGGTGTGCGCGTGGATCGGACCTGGAACTGGGCGAGACAGTGGAGCTGAAG 126

QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTriplePheGlnProArgGly 62

Db 127 TGCCAGGTGCTGCTGCCAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGCGCGCG 186

QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82

Db 187 GCGCGCGCGAGTCCCACTTCCTCTATATCTCCCAAAACAAGCCCAAGGCGCGCGAG 246

QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102

Db 247 GGCTGGACACCCAGCGGTTCTCGGCAAGAGGTGGGGACACCTTCGTCTCCACCTG 306

QY 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122

Db 307 AGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATC 366

QY 123 MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142

Db 367 ATGTACTTCAGGCACCTTCGTGCGGTCTTCCTGCCAGCGAAGCCCAACGAGCGCG 426

QY 143 ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162

Db 427 CCGCGACCAACACACCGCGGCCACCATCGGTGCGAGCCCTGTCCCTGCGCCAGAG 486

QY 163 AlaCysArgProAlaAlaGlyGlyAla----- 171

Db 487 GCGTGCAGCGCCAGCGCGGGGCGCGAGTGACACAGAGGGGTGGACTTCGCGCTGTGAT 546

QY 171 ----- 171

Db 547 ATCTACATCGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCACTGGTTATC 606

QY 172 -----GlyAsnArgArgArgValCysLysCysProArgProValVal 185

Db 607 ACCCTTTACTGCAACACAGGAAACCGAAGACGTGTTGCAAAAGTCCCGGCGCTGGTGC 666

QY 186 LysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198

Db 667 AAATCGGAGACAGCCAGCCTTTGCGCGAGATAGTGC 705

RESULT 6

DB121562

LOCUS

DEFINITION

DB121562 THYM2 Homo sapiens cDNA clone THYM2030213 5', mRNA

sequence.

ACCESSION

DB121562

VERSION

DB121562.1 GI:83141415

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1. (bases 1 to 549)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaquri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,K., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

16344560

CONTACT

Contact: Takao Isogai

FLJ Project (HRI Institute)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction; Helix Research Institute (HRI); 5'-end one pass sequencing; HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

Location/Qualifiers

source

1..549

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="THYM2030213"

/tissue_type="thymus"

/clone_lib="THYM2"

/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 3.09e-72 Length: 549

Score: 963.00 Matches: 181

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 92.3% Indels: 0

DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DB121562 (1-549)

QY 18 AlaAlaArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGlu 37

Db 5 GCGCGCAGCCCGAGCGAGTTCGGGGTGTCCGCTGGATCGGACCTGGGAACCTGGGCGAG 64

QY 38 ThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeu 57

Db 65 ACAGTGGAGTCAAGTGCAGGTGCTGTCTCAACCCGACGCTGGGCTGCTCTGGCTC 124

QY 58 PheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLys 77

Db 125 TTCCAGCGCGCGCGCGCGCGCGCTTCTCTCTCTATACCTCTCTCCCAAAACAAG 184

QY 78 ProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThr 97

Db 185 CCCAAGGCGCGCGAGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGGACACC 244

QY 98 PheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAla 117

Db 245 TTCGTCTCTCACCCTGAGCGACTTCGCGCAGAGAGACGAGGGCTACTATTCTCTCGGCC 304

QY 118 LeuSerAsnSerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysPro 137

Db 305 CTGAGCAACTCCATCATGTACTTACGCACTTCTGCGCGGTCTTCTCTGCGAGGAAGCCC 364

QY 138 ThrThrThrProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeu 157

Db 365 ACCACGACG 424

QY 158 SerLeuArgProGluAlaCysArgProAlaAlaGlyGlyValGlyAlaGlyAsnArgArgVal 177

Db 425 TCCCTGCGCGCCAGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484

QY 178 CysLysCysProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyr 197

Db 485 TGCAAAATGTCCCGCGCTGTGTGTTCAATCGGAGAGCAAGCCCGCGCTTTCGCGAGATAC 544

QY 198 Val 198

Db 545 GTC 547

RESULT 7

AL552456

LOCUS

DEFINITION

AL552456 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI070YG17 5-PRIME, mRNA sequence.

884 bp mRNA linear EST 30-MAR-2004

AL552456
 AL552456.3 GI:45857243
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 884)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31274271.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1670.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?&CSOD1070AD090Pl&c=1670.r.
 FEATURES
 source
 Location/Qualifiers
 1..884
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1070Y617"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,54e-71 Length: 884
 Score: 958.00 Matches: 195
 Percent Similarity: 98.5% Conservative: 0
 Best Local Similarity: 98.5% Mismatches: 3
 Query Match: 91.9% Indels: 3
 DB: 1 Gaps: 0
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 Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHieAlaAlaArg 20
 Db 71 ATGGCTTACAGTACCGCCCTTGCTCTGCGCTGGCTTCTGCTCCAGCCGCGAGG 130
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 131 CG-AGCCAGTTCCTGGGTTCGCGCTGGATCGGACCTGGAACCTGGCGAGACGTGGAG 189
 Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 190 CTGAGTGCAGGTGCTGTGTCTCAACCCGACGCTGGGCTGCTGTGGCTCTTCCAGCGG 249
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
 Db 250 CGCGGCGCGCGCGC-AGTCCCACTTCTCTCTATACCTCTCCCAAAACAAAGCCAGGCG 308
 Qy 81 AlaGluGlyLeuAspThrClnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 309 GCCGAGGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTGGGGACACCTTCGTCTTC 368
 Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
 Db 369 ACCCTGAGGAGCTTCGCGCGAGAGAACGAGGGGCTACTATTCTGCTCGGCCCTGAGCAAC 428

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 429 TCCATCATGTACTTTCAGCCACTTCTGTCGCGGTCTTCTCCGAGCAACCCACC-ACGACG 487
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 488 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGCAGCCCTGTCCCTGGCG 547
 Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaGlyAlaGlyAsnArgArgValCysLysCys 180
 Db 548 CCAGAGGCGTCCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
 Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 608 CCCCAGCGCTGTGTGTCAAATCGGAGACAAGCCAGCCCTTTCGCGGAGATACGTC 661
 RESULT 8
 DA931234
 LOCUS DA931234 SPLEN1 Homo sapiens cDNA clone SPLEN1000141 5', mRNA
 DEFINITION DA931234.1
 ACCESSION DA931234
 VERSION DA931234.1 GI:82056788
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 838)
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Teuriani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560
 Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.
 Location/Qualifiers
 1..838
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SPLEN1000141"
 /tissue_type="spleen"
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 /note="Vector: pME18SFL3"
 FEATURES
 source
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,23e-71 Length: 838
 Score: 952.50 Matches: 191
 Percent Similarity: 82.7% Conservative: 0
 Best Local Similarity: 82.7% Mismatches: 3
 Query Match: 91.3% Indels: 38
 DB: 9 Gaps: 1

US-10-804-763-3 (1-198) x DA931234 (1-838)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 89 ATGGCTTACCACTGACCGCTTGTCTCTGCGCTGGCTTGTCTCCACGCGCGCAG 148
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 149 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGACCTCGAACCTGGCGCAGACAGTGGAG 208
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 209 CTGAAGTGCAGGTGTCTGTCCACCCGACGTGGGCTGTCTGTGGCTCTTCCAGCG 268
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 269 CGCGGGCGCGCCAGTCCACCTTCTCTATATCTCTCCCAAAACAGCCCAAGCG 328
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 329 GCGAGGGGCTGACACCCAGCGGTCTCGGGCAAGAGGTGGGGACACCTTCGTCTC 388
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 389 ACCCTGAGCGACTTCGCCGAGAGAACGAGGGCTACTATTCTGCTGGCCCTGAGCAAC 448
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 449 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCCAGGAGGCCACACGAG 508
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 509 CCAGCGCCGCGACCAACACCGCGCGCACCATCGCTCGCAGCCCTGTCTCCCTCGC 568
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 569 CCAGAGCGGTGCGCGGCGCGCGGGGCGCAGTGCAACAGAGGGGTGGACTTCGCC 628
QY 171 ----- 171
Db 629 TGTGATATCTACATCTGGGGCGCTTGGCGGGACTTGTGGGTCTCTCTGTCTACTG 688
QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
Db 689 GGTATCACCTTTACTGNAACTACAGGAACCGAAGACGTGTTGCAAAATGTCGCG-CT 747
QY 184 ValValLysSerGlyAspLysProSerLeuSer 194
Db 748 GTGGTCNAATCGGGAGACAAGCCAGCCCTTCG 780

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RESULT 9

BI820267 882 bp mRNA linear EST 04-OCT-2001
 LOCUS 603036820F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5177885 5',
 DEFINITION mRNA sequence.

ACCESSION BI820267

VERSION BI820267.1 GI:15931817

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

1 (bases 1 to 882)

NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLML1443 row: g column: 06

High quality sequence stop: 769.

FEATURES
 Location/Qualifiers

1..882

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="IMAGE:5177885"

/lab_host="DH10B"

/clone_lib="NIH_MGC_115"

/note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27, and 1 male testis, age 69. Library is
 oligo-dr primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 5,5e-71 Length: 882
 Score: 951.50 Matches: 193
 Percent Similarity: 82.2% Conservatives: 1
 Best Local Similarity: 81.8% Mismatches: 2
 Query Match: 91.2% Indels: 40
 DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI820267 (1-882)

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QY 3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArgProSer 22
Db 65 ATACCAGTACCGCGCTTGTCTCGCGCTGGCTTGTCTCCACCGCGCGCGCAGC 124
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 125 CAGTTCCGGGTGTCCCGCTGGATCGGACTCGAACCTGGCGGAGACAGTGGAGCTGAAG 184
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 185 TGCCAGGTGCTGCTGTCCAAACCGACGTCGGCTGCTGTGCTCTTCCAGCGCGCGCG 244
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 245 GCCCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAACAAAGCCCAAGCGCGCGAG 304
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 305 GGGCTGGACACCCACGCGGTCTCGGGCAAGAGGTGGGGGACACCTTCTGTCTCACCCCTG 364
QY 103 SerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsnSerIle 122
Db 365 AGCGACTTCCGCGGAGAGACAGAGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATC 424
QY 123 MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db 425 ATGTACTTCAGCACTTCTGTGCGGTCTTCTCTCCAGCGAAGCCCAACACGCGCGCAGCG 484
QY 143 ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db 485 CGCGACCAACACCGCGCGCCACCATCGCGTCCGACGCCCTGTCCCTGCGCCCGCAGAG 544
QY 163 AlaCysArgProAlaAlaGlyGlyAla----- 171
Db 545 GGTGTCGCGCGCAGCGCGGGGGGCGCAGTGACACGAGGGGCTGGACTTTCGCTGTGAT 604
QY 171 ----- 171

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Db      605 ATCTACATCTGGCGCCCTTGGCGGACTTGTGGGTCCTTCTCTCTGCTACTGGTTAT 664
Qy      172 -----GlyAsnArgArgValCysLysCysProArgProValva 185
Db      665 CACCCTTTACTGCAACCAAGACCGAAGACGTTGTTGCAAAATGTCCTCCCGCTGTGGT 724
Qy      185 llySer-GlyAspLys-ProSerLeuSerAlaArgTyrVal 198
Db      725 CAAATCGGGGAGACAATGCCAGCCTTTTCGGCGAGATACGTC 766

RESULT 10
LOCUS   BI760947 780 bp mRNA linear EST 25-SEP-2001
DEFINITION 603043151F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
mRNA sequence.
ACCESSION BI760947
VERSION   BI760947.1 GI:15752525
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1458 row: e column: 13
High quality sequence start: 4
High quality sequence stop: 756.
Location/Qualifiers
1..780
organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183604"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,26e-70 Length: 780
Score: 943.50 Matches: 195
Percent Similarity: 82.6% Conservative: 0
Best Local Similarity: 82.6% Mismatches: 2
Query Match: 90.5% Indels: 41
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI760947 (1-780)

Qy      1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      67 ATGGCCTTACCAGTACCGCCCTTGTCTCTCGCGCTTGTCTGCTCCACGCCGCGCAG 126

```

```

Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTyrAsnLeuGlyGluThrValGlu 40
Db      127 CCAGACGAGTTCCGGGTGTCCCGCTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 186
Qy      41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrLeuPheGlnPro 60
Db      187 CTGAAGTGCAGGTGCTGCTGTCCAAACCCGACGTGGGGCTGCTGTGGCTCTTCCAGCG 246
Qy      61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      247 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 306
Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      307 GCCAGGGGGCTGGACACCCAGCGTTCTCGGGCAAGAGTTGGGGGACACCTTCTCTC 366
Qy      101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      367 ACCCTGACGACTTCCGCCGAGAGACGAGGGCTACTATTCTGCTCGGCTCTGAGCAAC 426
Qy      121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      427 TCCATCATGTACTTTCAGCCACTTCTGCGGGTCTTCTCTGCCAGGAGCCACCAACG 486
Qy      141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      487 CCAGCGCGCGACCAACACCCGCGGCCACCATCGCGTGGCAGCCCTGTCCCTGCGC 546
Qy      161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGly----- 172
Db      547 CCAGAGGGCTGCCGGCCAGCGCGGGGGGCGCAGT-GCACACGAGGGGGCTGGACTTCGC 605
Qy      172 ----- 172
Db      606 CTGTGATATATACATCTGGCGGCCCTTGGCGGGAGCTTGTGGGTCTTCTCTCTCACT 665
Qy      173 -----AsnArgArgArgValCysLysCysProArg 182
Db      666 TGGTTATCACCCTTTTACTGTCAACACAGGAAACCGAAGACGTGTTTGCAA-TGTCCCCG 724
Qy      183 ProValValLysSerGlyAspLysProSerLeu-SerAlaArgTyr 197
Db      725 CTTGTGTCAAATCGGAGACACGCCAGCCTTTTCGGCGAGATAC 770

RESULT 11
LOCUS   BX415859 1109 bp mRNA linear EST 03-MAY-2004
DEFINITION BX415859 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YC20
5-PRIME, mRNA sequence.
ACCESSION BX415859
VERSION   BX415859.2 GI:46957661
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1109)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
On May 15, 2003 this sequence version replaced gi:30767593.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1670.r

```

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSOCAP008BB10QPI&c=1670.r>.

FEATURES

source

Location/Qualifiers

1. .1109

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOCAP008YC20"

/tissue_type="THYMUS"

/clone_lib="Homo sapiens THYMUS"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 4,19e-69 Length: 1109
 Score: 931.00 Matches: 194
 Percent Similarity: 97.5% Conservative: 1
 Best Local Similarity: 97.0% Mismatches: 3
 Query Match: 89.3% Indels: 5
 DB: 4 Gaps: 0

US-10-804-763-3 (1-198) x BX415859 (1-1109)

QY 1 MetaLeuProValThrAla-LeuLeuLeuProLeuAla-LeuLeuLeuHisAlaAla 20
 Db 65 ATGGCTTACCAAGTACCCCTATGCTCTCGCGTGGCACTGCTGCTCCAGCGGCCA 124
 QY 20 rProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValG 40
 Db 125 GCGC-AGCCAGTTCGGGTGTCGCGCTGATCGACCTGGAACTGGCGGAGACAGTGG 183
 QY 40 luLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnP 60
 Db 184 AGCTGAAGTGCAGGCTGCTGTCTCAACCGACGTCGGGCTGCTGCTGCTTCCAGC 243
 QY 60 roArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysA 80
 Db 244 CGCGCGGCCGCCSC-AGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGG 302
 QY 80 laAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValL 100
 Db 303 CGGCGAGGGGCTGGACACCCAGCGTTCCTGGGCAAGAGGTTGGGGACACCTTCGTC 362
 QY 100 euThrLeuSerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerA 120
 Db 363 TCACCTGAGGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGGCCCTGAGCA 422
 QY 120 snSerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrT 140
 Db 423 ACTCATCATGTACTTACGCACTTCGTCGGCTTCTCTGCGGAGAGCCACC-ACGA 481
 QY 140 hrProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuA 160
 Db 482 CGCCAGCGCGGACCAACACCGCGGCCACCATCGCTCGGAGCCCTGTCCTGTC 541
 QY 160 rProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgArgValCysLysC 180
 Db 542 GCCCAGAGCGTGCCTGGCGCGGCGGCGGCGGCGGAGAACCGAAGACGCTGTTTGAAT 601
 QY 180 ysProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 602 GTCCCCGGCCTGTGTCAAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 657

RESULT 12

DA943842

LOCUS

DA943842 SPLEN2 Homo sapiens cDNA clone SPLEN2018853 5', mRNA
 linear EST 13-NOV-2005

DEFINITION

sequence.

ACCESSION

DA943842

VERSION

KEYWORDS

SOURCE

ORGANISM

DA943842.1 GI:82373467

EST.

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

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DA943842.1

GI:82373467

EST.

Homo sapiens

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GI:82373467

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Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes

TITLE

JOURNAL

PUBMED

COMMENT

Genome Res. 16 (1), 55-65 (2006)

16344560

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES

source

Location/Qualifiers

1..571

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="SPLEN2030425"

/tissue_type="spleen"

/clone_lib="SPLEN2"

/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 9,61e-67 Length: 571
Score: 899.00 Matches: 172
Percent Similarity: 98.9% Conservatives: 1
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 86.2% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DA952710 (1-571)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 35 ATGGCTTACCAAGTACCGCTTCTCTCGCGCTGGCTTCTCTCCACCGCCAGG 94
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 95 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 154
QY 41 LeuLysCysGlnValLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 155 CTGAAGTGCAGGTGCTGTCTTCCAAACCGACGCTGGGGTCTCTCTCTCCAGCGG 214
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 215 CGCGGGCGCGCGCCAGTCCGACCTCTCTCTATACCTCTCCAAAACAGCCCGAGGG 274
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 275 GCCGAGGGGCTGCACACCCAGCGGTTCGGGCAAGAGGTTGGGGACACCTTCGTCTC 334
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 335 ACCCTGAGGACGCTTCGGCGAGAGAACGAGGGCTACTATTCTCTCGGCCCTGAGCAAC 394
QY 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 395 TCATCATGTACTTCAGGCACCTTCGTCCGCGTCTCTCTCCAGCGAAGCCACACGAGC 454
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 455 CCAGCGCGCGCGACCAACCGCGCCACCATCGCTCGCAGCCCTGTCTCTCGCGC 514
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArg 175
Db 515 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGCGCAGTGCACACGAGG 559

RESULT 15

DA826683

LOCUS

DEFINITION

sequence.

DA826683

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology

Developmental Organization, Japan); cDNA library construction:

Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,

Research Association for Biotechnology (RAB) and Biotechnology

Center, National Institute of Technology and Evaluation; 3'-end one

pass sequencing: RAB.

Location/Qualifiers

1..576

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PERIC2008112"

/tissue_type="pericardium"

/clone_lib="PERIC2"

/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 9,72e-67 Length: 576

Score: 899.00 Matches: 172

Percent Similarity: 98.9% Conservatives: 1

Best Local Similarity: 98.3% Mismatches: 2

Query Match: 86.2% Indels: 0

DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DA826683 (1-576)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 36 ATGGCTTACCAAGTACCGCTTCTCTCGCGCTGGCTTCTCTCCACCGCCAGG 95

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 96 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 155

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QY 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db |||||
156 CTGAAGTGCCAGGTGCTGTGTCCAAACCGACGTCGGGCTGCTCGTGCTCTTCCAGCG 215
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db |||||
216 CGCGGCGCGCGCGCAGTCCACCTTCCTCTATACCTTCCCAAAACAAGCCCAAGCG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db |||||
276 GCCGAGGGGCTGGACACCCAGCGTTCCTCGGCAGAGGTTGGGGACACCTTCGTCTC 335
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db |||||
336 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAAC 395
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db |||||
396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCCTGCCAGCGAAGCCACACGACG 455
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db |||||
456 CCAGCGCGCGNACCACACACCGCGGCCCATCGCTGCGACGCCCTGTCTCTGCGC 515
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArg 175
Db |||||
516 CCAGAGGCGTGC CGGCCAGCGCGGGGGCGCGCAGTGCAACAGAGG 560
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Search completed: May 30, 2006, 06:51:27
Job time : 4306.33 secs

SEQUENCE COMPARISON 1 of 9/6/06

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2006, 21:45:26 ; Search time 2523 Seconds
(without alignments)
6248.218 Million cell updates/sec

Title: US-10-804-763-2
Perfect score: 2261
Sequence: 1 gaatacaggctccggcgccgg.....aaaaaaaaaaaaaaaaaaaaa 2261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_8.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002as.*
 - 7: Geneseqn2002bs.*
 - 8: Geneseqn2003as.*
 - 9: Geneseqn2003bs.*
 - 10: Geneseqn2003cs.*
 - 11: Geneseqn2003ds.*
 - 12: Geneseqn2004as.*
 - 13: Geneseqn2004bs.*
 - 14: Geneseqn2005s.*
 - 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 2261 | 100.0 | 2261 | ADP10406 | Adp10406 Reference |
| 2 | 2261 | 100.0 | 2261 | ADP92791 | Adp92791 Nucleotid |
| 3 | 2261 | 100.0 | 2261 | ADP19437 | Adp19437 DNA of th |
| 4 | 2261 | 100.0 | 2261 | ADW86779 | Adw86779 Human CD8 |
| 5 | 2261 | 100.0 | 2261 | ADZ26401 | Adz26401 Human CD8 |
| 6 | 2132.8 | 94.3 | 3048 | ADQ64633 | Adq64633 Novel hum |
| 7 | 2061.6 | 91.2 | 2134 | ADQ22926 | Adq22926 Human sof |
| 8 | 2061.2 | 91.2 | 2123 | ADP90782 | Adp90782 Human hep |
| 9 | 2029 | 89.7 | 2150 | ADP92793 | Adp92793 cDNA of a |
| 10 | 2029 | 89.7 | 2150 | ADP19439 | Adp19439 Human sec |
| 11 | 2029 | 89.7 | 2150 | ADZ26403 | Adz26403 Human CD8 |
| 12 | 1905 | 84.3 | 3518 | ADP96282 | Adp96282 Human C-r |
| 13 | 1821 | 80.5 | 3476 | ADP96284 | Adp96284 Human C-r |
| 14 | 1683 | 74.4 | 3407 | ADP96285 | Adp96285 Human C-r |
| 15 | 1683 | 74.4 | 3743 | ADP96281 | Adp96281 Human C-r |
| 16 | 1393 | 61.6 | 4392 | ADP96283 | Adp96283 Human C-r |
| 17 | 1361.4 | 60.2 | 1729 | ADQ18424 | Adq18424 Human sof |
| 18 | 1361.4 | 60.2 | 1729 | ACF87521 | Acf87521 Human SIR |

| | | | | | | |
|----|-------|------|------|----|----------|---------------------|
| 19 | 1048 | 46.4 | 1060 | 2 | AAQ57986 | Aaq57986 Genomic s |
| 20 | 1048 | 46.4 | 1060 | 10 | ADD25612 | Add25612 Binding d |
| 21 | 1048 | 46.4 | 1060 | 11 | AD131688 | Adi131688 Human CDN |
| 22 | 1048 | 46.4 | 1060 | 13 | ADS83755 | Ads83755 Human lym |
| 23 | 761.4 | 33.7 | 773 | 3 | AAZ29002 | Aaz29002 Human CD8 |
| 24 | 744 | 32.9 | 744 | 14 | AED96294 | Aed96294 Human C-r |
| 25 | 708 | 31.3 | 708 | 2 | AXX80967 | Aax80967 Human CD8 |
| 26 | 706 | 31.3 | 708 | 8 | ABZ69260 | Abz69260 Human CD8 |
| 27 | 708 | 31.3 | 708 | 13 | ADS92817 | Ads92817 Nucleotid |
| 28 | 708 | 31.3 | 708 | 13 | ADS19462 | Ads19462 Coding se |
| 29 | 708 | 31.3 | 708 | 14 | ADV42461 | Adv42461 Human psy |
| 30 | 708 | 31.3 | 708 | 15 | AEF68357 | Aef68357 Human CD8 |
| 31 | 704.8 | 31.2 | 708 | 8 | ABZ69262 | Abz69262 Human CD8 |
| 32 | 676 | 29.9 | 727 | 10 | ADF90668 | Adf90668 Human hep |
| 33 | 646.4 | 28.6 | 662 | 12 | ADN11772 | Adn11772 Human CD8 |
| 34 | 644.4 | 28.5 | 1637 | 12 | ADN11778 | Adn11778 CD8-NS2/3 |
| 35 | 644.4 | 28.5 | 2909 | 12 | ADN11779 | Adn11779 CD8-NS2/3 |
| 36 | 610.4 | 27.0 | 708 | 13 | ADS92815 | Ads92815 Nucleotid |
| 37 | 610.4 | 27.0 | 708 | 13 | ADS19461 | Ads19461 DNA of th |
| 38 | 610 | 27.0 | 610 | 12 | ADO41257 | Ado41257 Human CDN |
| 39 | 593 | 26.2 | 610 | 13 | ADU12274 | Adu12274 Solid tum |
| 40 | 586 | 25.9 | 599 | 12 | ADO41256 | Ado41256 Human cDN |
| 41 | 557.4 | 24.7 | 2001 | 13 | ADS92807 | Ads92807 Nucleotid |
| 42 | 557.4 | 24.7 | 2001 | 13 | ADS19453 | Ads19453 DNA of th |
| 43 | 552 | 24.4 | 1891 | 13 | ADS92809 | Ads92809 Nucleotid |
| 44 | 552 | 24.4 | 1891 | 13 | ADS19455 | Ads19455 DNA of th |
| 45 | 543 | 24.0 | 1131 | 3 | AAZ46253 | Aaz46253 cDNA enco |

ALIGNMENTS

RESULT 1
ADP10406
ID ADP10406 standard; DNA; 2261 BP.
XX
AC ADP10406;
XX
DT 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequences for marker probe #83.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
OS Homo sapiens.
XX
PN WQ2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
DR WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 80; SEQ ID NO 415; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The

transplant only
see
note

SEQUENCE COMPARISON 1 of 9/6/06

methods, system and kits are useful in diagnosing or monitoring
transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
islet, lung, bone marrow or stem cell transplant rejection,
xenotransplant rejection or mechanical organ replacement rejection, in an
individual. The method is also useful in assessing the immune status of
an individual. The methods are also useful in diagnosing and monitoring
diseases that involve the immune system, e.g. rheumatoid arthritis,
lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
bacterial or fungal infection. The present sequence represents a
mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
and monitoring of allograft rejection and other disorders.

XX Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 12; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAGGCTCCGGCCGGCGGCGAAGGGCGCAACTTTCCCTCGGCGCCCAACGGCT 60
DB 1 GAAATCAGGCTCCGGCCGGCGGCGAAGGGCGCAACTTTCCCTCGGCGCCCAACGGCT 60

QY 61 CCGCGCGGCTCCCTCGGCGCGGCGGAGCTTCGAGCCAGCAGCGTCTGGGGAGCGGTC 120
DB 61 CCGCGCGGCTCCCTCGGCGCGGCGGAGCTTCGAGCCAGCAGCGTCTGGGGAGCGGTC 120

QY 121 TGGCCCTTACAGTGACCGGCTTGTCTCGCGCTGGCTTGTCTTCACCGCGCGAGGC 180
DB 121 TGGCCCTTACAGTGACCGGCTTGTCTCGCGCTGGCTTGTCTTCACCGCGCGAGGC 180

QY 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAGC 240
DB 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAGC 240

QY 241 TGAAGTGCCAGGTGCTGCTCCAAACCGAGCTCGGGCTGCTGCTGGCTTTCCAGCGCG 300
DB 241 TGAAGTGCCAGGTGCTGCTCCAAACCGAGCTCGGGCTGCTGCTGGCTTTCCAGCGCG 300

QY 301 GCGGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCCCAAACAGCCCAAGGGCGG 360
DB 301 GCGGCGCGCGCGAGTCCACCTTCTCTCTATATCTTCCCAAACAGCCCAAGGGCGG 360

QY 361 CGAGGGGCTGACACCGAGCGGTTCTCGGGAAGAGGTTGGGGGACACCTTCGCTCTCA 420
DB 361 CGAGGGGCTGACACCGAGCGGTTCTCGGGAAGAGGTTGGGGGACACCTTCGCTCTCA 420

QY 421 CCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTCTCGCTCGGCGCTGAGCACT 480
DB 421 CCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTCTCGCTCGGCGCTGAGCACT 480

QY 481 CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTCGCAGCGAAGCCCAACGAGCG 540
DB 481 CCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTCGCAGCGAAGCCCAACGAGCG 540

QY 541 CAGCGCGCGAGCACCAACACCGCGCGCCCAACATCGCGTCCGAGCGCCCTGTCCGCGC 600
DB 541 CAGCGCGCGAGCACCAACACCGCGCGCCCAACATCGCGTCCGAGCGCCCTGTCCGCGC 600

QY 601 CAGAGCGCTGCCGCGCGGCGGCGGCGAGTGCACACGAGGGGCTGGACTTCGCT 660
DB 601 CAGAGCGCTGCCGCGCGGCGGCGGCGAGTGCACACGAGGGGCTGGACTTCGCT 660

QY 661 GTGATATCTACATCTGGGCGGCTTGGCGGAGCTTGTGGGGTCTTCTCTGTCACTGG 720
DB 661 GTGATATCTACATCTGGGCGGCTTGGCGGAGCTTGTGGGGTCTTCTCTGTCACTGG 720

QY 721 TTATACCCCTTTACTGCAACACGAGAACCGAAGACGTGTTTCAAAATGTCCCGGCGCTG 780
DB 721 TTATACCCCTTTACTGCAACACGAGAACCGAAGACGTGTTTCAAAATGTCCCGGCGCTG 780

QY 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTTCGGCGAGATACGTTAAACCTGTGCAACAG 840
DB 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTTCGGCGAGATACGTTAAACCTGTGCAACAG 840

841 CCACATACATTACTTCAAACTGAGATCCTTCTCTTTTGGGGAGCAAGTCTCTCCCTTTTAT 900
841 CCACATACATTACTTCAAACTGAGATCCTTCTCTTTTGGGGAGCAAGTCTCTCCCTTTTAT 900

901 TTTTTCAGTCTTCTCCTCGTGTATTCATTCTCATGATTATTTATTTAGTGGGGCGGG 960
901 TTTTTCAGTCTTCTCCTCGTGTATTCATTCTCATGATTATTTATTTAGTGGGGCGGG 960

961 GTGGGAAAGATTACTTTTTTCTTTATGTGTGTGACGGGAAACAAAATAAGTAAATCTAC 1020
961 GTGGGAAAGATTACTTTTTTCTTTATGTGTGTGACGGGAAACAAAATAAGTAAATCTAC 1020

1021 AGTACACCAAGGGTCACAATACATCTGTTGTGCGCATCGCGTAGGGGTGCGAAAGGGG 1080
1021 AGTACACCAAGGGTCACAATACATCTGTTGTGCGCATCGCGTAGGGGTGCGAAAGGGG 1080

1081 CAGGCGAGAGTACCCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCCATG 1140
1081 CAGGCGAGAGTACCCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGGAGGACCCCATG 1140

1141 CCATCTCAACCTTCTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT 1200
1141 CCATCTCAACCTTCTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT 1200

1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260

1261 GCTCAGGCTCTTCTCTCCACACCACTTCAAGTCTTTTCTTCCGAGGCGCTGTCTCAGG 1320
1261 GCTCAGGCTCTTCTCTCCACACCACTTCAAGTCTTTTCTTCCGAGGCGCTGTCTCAGG 1320

1321 TGAGTGCTTGAAGTCTCCAGCGCAAGGAACTGCTTCTGATACCTGGGATCTGT 1380
1321 TGAGTGCTTGAAGTCTCCAGCGCAAGGAACTGCTTCTGATACCTGGGATCTGT 1380

1381 GCCCAGAGCTTCGAGGAGTAAAGTAAAGAGAGAACTGCTTTCGAGAGTCTTAT 1440
1381 GCCCAGAGCTTCGAGGAGTAAAGTAAAGAGAGAACTGCTTTCGAGAGTCTTAT 1440

1441 AATGTAACAAATATCAGACTTTTTTTTTTATAATCAAGCCTTAAATTTGATAGACCTAA 1500
1441 AATGTAACAAATATCAGACTTTTTTTTTTATAATCAAGCCTTAAATTTGATAGACCTAA 1500

1501 AATAAATGAAGTGTGAGCTTAAACCTTGAAGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
1501 AATAAATGAAGTGTGAGCTTAAACCTTGAAGAAATGAATCCCTCTATCTCTAAAGAAAT 1560

1561 CTCTGTGAACCCCTATGTGGAGGGGAATGCTCTCCAGGCGCTTGCATTCGAGGGG 1620
1561 CTCTGTGAACCCCTATGTGGAGGGGAATGCTCTCCAGGCGCTTGCATTCGAGGGG 1620

1621 CCCATGAAGAGGACAGGCTACCCCTTACAAATAGAAATTTGAGCATCAGTCAAGTTAAA 1680
1621 CCCATGAAGAGGACAGGCTACCCCTTACAAATAGAAATTTGAGCATCAGTCAAGTTAAA 1680

1681 CTAAGGCGCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTCTCGGATCACTGATGA 1740
1681 CTAAGGCGCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTCTCGGATCACTGATGA 1740

1741 CTTTTTATATTTGTAAGACAAATTTGTTGGAGAGCCCTCACACAGCCCTGCGCTCTGCT 1800
1741 CTTTTTATATTTGTAAGACAAATTTGTTGGAGAGCCCTCACACAGCCCTGCGCTCTGCT 1800

1801 CAACTAGCAGATACAGGGATGAGGAGACCTGACTCTCTTAAAGAGGCTGAGAGGCCAAA 1860
1801 CAACTAGCAGATACAGGGATGAGGAGACCTGACTCTCTTAAAGAGGCTGAGAGGCCAAA 1860

1861 CTGCTGTCCCAACATGCACTTCTTGTCTTAAAGTATGTTACAAAGCAATTCCTGCCCAT 1920
1861 CTGCTGTCCCAACATGCACTTCTTGTCTTAAAGTATGTTACAAAGCAATTCCTGCCCAT 1920

SEQUENCE COMPARISON 1 of 7/6/06

Wed May 31 15:00:25 2006

us-10-804-763-2.rng

1921 GGAGAGAAAAA... 1980
1921 GGAGAGAAAAA... 1980
1981 AATAATCTCTGTTAATATGGTGTACATCTCTTCCTGATTATTTCTACACATACATGTA 2040
1981 AATAATCTCTGTTAATATGGTGTACATCTCTTCCTGATTATTTCTACACATACATGTA 2040
2041 AATATGCTCTCTTTTAAATAGGTTGTACTATGCTGTGTATGAGTGGCTTTAATGAAT 2100
2041 AATATGCTCTCTTTTAAATAGGTTGTACTATGCTGTGTATGAGTGGCTTTAATGAAT 2100
2101 AAACATTTGTAGCATCTCTTTAATGGTGTAAACAGCAAAAAA 2160
2101 AAACATTTGTAGCATCTCTTTAATGGTGTAAACAGCAAAAAA 2160
2161 AAAAAA 2220
2161 AAAAAA 2220
2221 AAAAAA 2261
2221 AAAAAA 2261

RESULT 2
ADS92791
ID ADS92791 standard; cDNA; 2261 BP.
XX AC ADS92791;
XX DT 16-DEC-2004 (first entry)
XX DE Nucleotide sequence of a CD8 alpha-chain protein.
XX KW immune response; cell-specific antigen; alloantigen; CD8;
XX KW CD8 alpha-chain; cellular immune response; humoral immune response;
XX KW transplant allograft; graft-versus-host disease; transplant; gene; ss.
XX OS Homo sapiens.

Handwritten signature

Location/Qualifiers
120..827
/*tag= a
/product= "CD8 alpha-chain"

WO2004083244-A2.
30-SEP-2004.
19-MAR-2004; 2004WO-US008574.
19-MAR-2003; 2003US-0456378P.
(ISOG-) ISOGENIS INC.
Qi Y, Zhang X, Konigsberg PJ;
WPI; 2004-691022/67.
P-PSDB; ADS92790.
Specifically inhibiting host immune responses to alloantigens, useful for e.g. treating graft-versus-host disease, comprises contacting a target cell expressing the antigen with an expression vector encoding a CD8 polypeptide.
Disclosure; Fig 1; 98pp; English.

The specification describes a method for specifically inhibiting a host immune response to target cell-specific antigens (e.g. alloantigens). The method comprises contacting a target cell expressing the antigen with an expression vector encoding a CD8 polypeptide comprising the CD8 alpha-chain, where the CD8 polypeptide is expressed by the target cell and

where the host immune response against the target cell is specifically inhibited. The method of the invention is useful for specifically inhibiting both cellular and humoral immune responses to alloantigens, thus finding use in extending the survival of transplant allografts, in treating graft-versus-host disease in transplant recipients. The present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha-chain may be used in the method of the invention.

Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 13; Length 2261;
Best Local Similarity 100.0%; Pred. NO. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAGGCTCCGGCCGCGCGCAAGGCGCAACTTTCCCTCTCGCGCCCAACCGGCT 60
Db 1 GAAATCAGGCTCCGGCCGCGCGCAAGGCGCAACTTTCCCTCTCGCGCCCAACCGGCT 60
QY 61 CCCGCGCGCTCCCTCCGCGCGCGAGCTTCGAGCCAGAGCGCTCTCGGGAGCGCGTCA 120
Db 61 CCCGCGCGCTCCCTCCGCGCGCGAGCTTCGAGCCAGAGCGCTCTCGGGAGCGCGTCA 120
QY 121 TGGCTTTACAGTGACCGCTTGTCTCTGCGCGTGGCTTGTCTCTCCAGCGCCGAGGC 180
Db 121 TGGCTTTACAGTGACCGCTTGTCTCTGCGCGTGGCTTGTCTCTCCAGCGCCGAGGC 180
QY 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTTGGAACTTGGCGGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCGGGCTGTCGCGCTGGATCGGACCTTGGAACTTGGCGGAGACAGTGGAGC 240
QY 241 TGAAGTGCCAGTGCTGTGTCTCAACCGAGCTGGGCTGTCTGTGGCTTTCCAGCCGC 300
Db 241 TGAAGTGCCAGTGCTGTGTCTCAACCGAGCTGGGCTGTCTGTGGCTTTCCAGCCGC 300
QY 301 GGGCGCGCGCGCCAGTCCCACTTCTCTCTTATCTCTCTCCCAAAACAGCCCAAGCGCG 360
Db 301 GGGCGCGCGCGCCAGTCCCACTTCTCTCTTATCTCTCTCCCAAAACAGCCCAAGCGCG 360
QY 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGGAAGAGGTTGGGGGACACTTTCGCTCTCA 420
Db 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGGAAGAGGTTGGGGGACACTTTCGCTCTCA 420
QY 421 CCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCTCGCGCCCTGAGCAACT 480
Db 421 CCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCTCGCGCCCTGAGCAACT 480
QY 481 CCATCATGTACTTACGCCACTTCTGTGCGGTTCTCTGCCAGCAAGCCCAACAGCGC 540
Db 481 CCATCATGTACTTACGCCACTTCTGTGCGGTTCTCTGCCAGCAAGCCCAACAGCGC 540
QY 541 CAGCGCGCGGACCAACACCGCGCGCGCCAGTGCACAGAGGGGCTGAGCTTCGCT 600
Db 541 CAGCGCGCGGACCAACACCGCGCGCGCCAGTGCACAGAGGGGCTGAGCTTCGCT 600
QY 601 CAGAGGGCTGCGCGCGCGCGCGCGCGAGTGCACAGAGGGGCTGAGCTTCGCT 660
Db 601 CAGAGGGCTGCGCGCGCGCGCGCGCGAGTGCACAGAGGGGCTGAGCTTCGCT 660
QY 661 GTGATATCTACATCTGGCGCGCCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCACCTG 720
Db 661 GTGATATCTACATCTGGCGCGCCCTTGGCGCGGACTTGTGGGGTCTCTCTCTGTCACCTG 720
QY 721 TTATCACCCTTTACTGCAACCAACAGGAAACCGAGAGCGTGTGTGCAAAATGTCCCGGCTG 780
Db 721 TTATCACCCTTTACTGCAACCAACAGGAAACCGAGAGCGTGTGTGCAAAATGTCCCGGCTG 780
QY 781 TGGTCAAAATCGGAGACAAGCCAGCTTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAGCCAGCTTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 840
QY 841 CCATCATATTACTTCAAACTGAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTTTCA 900
Db 841 CCATCATATTACTTCAAACTGAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTTTCA 900

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